

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 01:26:57 ; Search time 3770 Seconds
(without alignments)
12035.175 Million cell updates/sec

Title: U67963
Perfect score: 1192
Sequence: 1 CCAGCCCGAAGGCGAGGTC.....CAAAAAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1102	92.4	1141	3	CR622559	full-leng
2	909.2	76.3	1117	5	BM924140	AGENCOURT
3	886	74.3	961	5	BM924140	AGENCOURT
4	882.6	74.0	926	5	BM924140	AGENCOURT
5	863.4	72.4	1011	5	BM924140	AGENCOURT
6	862	72.3	988	5	BM924140	AGENCOURT
7	860.8	72.2	912	5	BM924140	AGENCOURT
8	842.2	70.7	848	5	BM924140	AGENCOURT
9	839.6	70.4	944	5	BM924140	AGENCOURT
10	802.6	67.3	896	5	BM924140	AGENCOURT
11	788.4	66.1	815	7	BM924140	AGENCOURT
12	783.4	65.7	878	5	BM924140	AGENCOURT
13	772.2	64.8	916	5	BM924140	AGENCOURT
14	768.8	64.5	806	4	BM924140	AGENCOURT
15	765.8	64.2	885	5	BM924140	AGENCOURT
16	763.2	64.0	906	6	BM924140	AGENCOURT
17	760.4	63.8	869	4	BM924140	AGENCOURT
18	758.2	63.6	794	4	BM924140	AGENCOURT
19	753.8	63.2	989	5	BM924140	AGENCOURT
20	752.2	63.1	880	5	BM924140	AGENCOURT
21	750	62.9	793	5	BM924140	AGENCOURT
22	748	62.8	916	4	BM924140	AGENCOURT
23	742.6	62.3	889	4	BM924140	AGENCOURT
24	740	62.1	781	5	BM924140	AGENCOURT

25	736.8	61.8	855	4	BM924140	AGENCOURT
26	735.4	61.7	905	5	BM924140	AGENCOURT
27	732.4	61.4	876	5	BM924140	AGENCOURT
28	725.8	60.9	917	4	BM924140	AGENCOURT
29	715.8	60.1	856	5	BM924140	AGENCOURT
30	713	59.8	867	5	BM924140	AGENCOURT
31	712.4	59.8	947	5	BM924140	AGENCOURT
32	704.4	59.1	978	5	BM924140	AGENCOURT
33	701	58.8	1160	4	BM924140	AGENCOURT
34	690.8	58.0	1107	3	BM924140	AGENCOURT
35	689	57.8	689	4	BM924140	AGENCOURT
36	683.4	57.3	946	4	BM924140	AGENCOURT
37	683	57.3	870	5	BM924140	AGENCOURT
38	681.2	57.1	891	5	BM924140	AGENCOURT
39	675.2	56.6	863	5	BM924140	AGENCOURT
40	673.8	56.5	896	5	BM924140	AGENCOURT
41	665.2	55.8	1134	4	BM924140	AGENCOURT
42	663.6	55.7	936	5	BM924140	AGENCOURT
43	662	55.5	662	6	BM924140	AGENCOURT
44	659.8	55.4	709	2	BM924140	AGENCOURT
45	658.6	55.3	910	5	BM924140	AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS CR622559 1141 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI019YD19 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR622559
VERSION CR622559.1 GI:50503366
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1141)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: flianglifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1141)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1..1141
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI019YD19"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 92.4%; Score 1102; DB 3; Length 1141;
Best Local Similarity 100.0%; Pred. No. 11e-287;
Matches 1102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CCAGCCCGAAGGCGAGGTCGGTGGGGGAGAGGGCTCGGAGCTCGCTTCCTGCTGCC 60
DB 40 CCAGCCCGAAGGCGAGGTCGGTGGGGGAGAGGGCTCGGAGCTCGCTTCCTGCTGCC 99

QY 61 TTGGGGCCGCCAGATGAGGNAACAGCCCGATTTCCTGGTTCGTATTCCTCAGGCTGTC 120
Db 100 TTGGGGCCGCCAGATGAGGNAACAGCCCGATTTCCTGGTTCGTATTCCTCAGGCTGTC 159
QY 121 GTGGTTGTGGAAATGCAACGCCAGCACATAATGGAACAGAGACCTTGAAGACCTTCCAGC 180
Db 160 GTGGTTGTGGAAATGCAACGCCAGCACATAATGGAACAGAGACCTTGAAGACCTTCCAGC 219
QY 181 ATGCCAGAGGAAGTTCCCCAGGCGGACCCCGCAGAGCATTCCTTACCAGGACCTCCCT 240
Db 220 ATGCCAGAGGAAGTTCCCCAGGCGGACCCCGCAGAGCATTCCTTACCAGGACCTCCCT 279
QY 241 CACCTGGTCAATGCAGACGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGACACA 300
Db 280 CACCTGGTCAATGCAGACGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGACACA 339
QY 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCGGAGAGACAGTGGCGCGTATGAAGAG 360
Db 340 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCGGAGAGACAGTGGCGCGTATGAAGAG 399
QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGTGTTCGCCACGACCATGTTGGCCAC 420
Db 400 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGTGTTCGCCACGACCATGTTGGCCAC 459
QY 421 GGACAGCGGAGGAGGAGGATGCTAGTGTCTGACTTCCAGCTTTTCGTGAGGATGTG 480
Db 460 GGACAGCGGAGGAGGAGGATGCTAGTGTCTGACTTCCAGCTTTTCGTGAGGATGTG 519
QY 481 TTGCAGCATGTGGATTTCATGCAGAAAGACTACCTCGGCTTCCTGTCTTCTCTGGGC 540
Db 520 TTGCAGCATGTGGATTTCATGCAGAAAGACTACCTCGGCTTCCTGTCTTCTCTGGGC 579
QY 541 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCCGAGAGAGCGCGGCCACTTTCGCC 600
Db 580 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCCGAGAGAGCGCGGCCACTTTCGCC 639
QY 601 GGCATGTTACTCATTTTCGCTTCTGTTCTTGGCAATCTGTAATCTGGAACAACTTCAAG 660
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QY 661 GTCTTTGCTGCGAAAGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCGCCATCGAC 720
Db 700 GTCTTTGCTGCGAAAGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCGCCATCGAC 759
QY 721 TCCAGCGTCTCTTCGGAATAAGACAGAGTTCGACATTTTAACTCAGACCCCTGATC 780
Db 760 TCCAGCGTCTCTTCGGAATAAGACAGAGTTCGACATTTTAACTCAGACCCCTGATC 819
QY 781 TGCCGGCAGGCGTGAAGTGTCTTTCGGCATCCAACTGCTGMAATGCCGTCTCAGGGTG 840
Db 820 TGCCGGCAGGCGTGAAGTGTCTTTCGGCATCCAACTGCTGMAATGCCGTCTCAGGGTG 879
QY 841 GAGCGCGCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCGGATCGC 900
Db 880 GAGCGCGCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCGGATCGC 939
QY 901 CTATGTGACAGAAAGGGGCTTACCTGCTCATGAGTTAGCCAGAGCAGCAGCAAGACT 960
Db 940 CTATGTGACAGAAAGGGGCTTACCTGCTCATGAGTTAGCCAGAGCAGCAGCAAGACT 999
QY 961 CTCAGATTTATGAGTGCCTTACCATGTTCTTCCACAGGAGCTTCTTGAAGTCAACCAAC 1020
Db 1000 CTCAGATTTATGAGTGCCTTACCATGTTCTTCCACAGGAGCTTCTTGAAGTCAACCAAC 1059
QY 1021 TCCGTTCTTCCATGAAATAAATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAAGTTCG 1080
Db 1060 TCCGTTCTTCCATGAAATAAATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAAGTTCG 1119
QY 1081 TCCCCACCTGAAATGCAATTGGC 1102
Db 1120 TCCCCACCTGAAATGCAATTGGC 1141

RESULT 2
BX403703
LOCUS
DEFINITION BX403703 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA009ZC10
5-PRIME, mRNA sequence.
ACCESSION BX403703
VERSION BX403703.2 GI:46929030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1117)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30643737.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1117
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA009ZC10"
/tissue_type="PLACENTA"
/note="vvector; pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 76.3%; Score 909.2; DB 5; Length 1117;
Best Local Similarity 93.6%; Pred. No. 2.5e-235;
Matches 970; Conservative 9; Mismatches 52; Indels 5; Gaps 3;
QY 158 CAGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCCAGGCGGACCCCGCAGA 217
Db 84 CCGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCCAGGCGGACCCCGCAGA 143
QY 218 GCATTCTCTACAGGACCTCCCTCACCTGCTCANTGCAGAGGACAGTACCTCTTCTGCA 277
Db 144 GCATTCTCTACAGGACCTCCCTCACCTGCTCAATGCAGAGGACAGTACCTCTTCTGCR 203
QY 278 GGTACTGGAACCCACAGGCACACCCCAAGGCCCTCATCTTGTGTCCTCATGAGCCGGAG 337
Db 204 GGTACTGGAACCCACAGGCACACCCCAAGGCCCTCATCTTGTGTCCTCATGAGCCGGAG 263
QY 338 AGCAGTGGCCGCTATGAAGAGCTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGT 397
Db 264 AGCAGTGGCCGCTATGAAGAGCTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGT 323
QY 398 TCGCCACGACCATGTTGGCCACGACAGAGCGAAGGGAGAGATGGTAGTCTGACT 457
Db 324 TCGCCACGACCATGTTGGCCACGACAGAGCGAAGGGAGAGATGGTAGTCTGACT 383
QY 458 TCCACGTTTTCGTTCAGGATGTGTTGCAGCATGTGGATTCCATCAGAAAGACTACCCCTG 517
Db 384 TCCACGTTTTCGTTCAGGATGTGTTGCAGCATGTGGATTCCATCAGAAAGACTACCCCTG 443
QY 518 GGTTCCTCTGCTTCTCTCTGGCCACTCCCATTGGAGGCGGCATCGCCATCTCTACGGCG 577
Db 444 GGTTCCTCTGCTTCTCTCTGGCCACTCCCATTGGAGGCGGCATCGCCATCTCTACGGCG 503

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QY 578 CAGAGAGCGCGGCACCTTCGCGGCATGGTACTCATTTGCGCTCTGGTCTTGCCAATC 637
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Db 504 CAGAGAGCGCGGCACCTTCGCGGCATGGTACTCATTTGCGCTCTGGTCTTGCCAATC 563
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QY 638 CTGAATCTGCAACAACATTTCAAGGTCTTCTGCGGAAAGTGTCAACCTTGCTGCGCAA 697
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Db 564 CTGAATCTGCAACAACATTTCAAGGTCTTCTGCGGAAAGTGTCAACCTTGCTGCGCAA 623
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QY 698 ACTTGTCCTCGCGGCCATCGACTCTCAGCGTCTCTCGGAATGAAGACAGAGGTCGACA 757
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Db 624 ACTTGTCCTCGCGGCCATCGACTCTCAGCGTCTCTCGGAATGAAGACAGAGGTCGACA 683
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QY 758 TTATAACTCAGACCCCTGATCTCGCGGCAGGGCTGAAGTGTGCTTCGCGCATCCAAAC 817
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Db 804 TGCTCAGGGCTCTCGCGATCGCTATGTGACAGCAAGGGCCCTACCTGCTCATGGAGT 863
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QY 938 TAGCCAAGAGCGCAGACAGACTCTCAAGATTTATGAAGTGCCTACCATGTTCTCCACA 997
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Db 864 TAGCCAAGAGCGCAGGCAAGACTCTCAAGATTTATGAAGTGCCTCCATGTTCTCCACA 923
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QY 998 AGGAGCTTCTGAAGTCAACAACTCGTCTTCATGAAATAAAGTGGTCTCTC-AA 1056
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Db 924 AGGAGCTTCTGAAGTCAACAACTCGTCTTCATGAGAAAGTGGTCTCTC-A 983
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QY 1057 AGGAGCGCAGGCAAGACTCGTCTCCACCTGATGCAATGCAATGCGCGTCCCGGCTCA 1116
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Db 984 AGGAGCGCAGGCAAGACTCGTCTCCACCTGATGCAATGCAATGCGCGTCCCGGCTCA 1039
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QY 1117 TGGTCTGGGGATCAGGCGGAGGAGGAGGAGATGGTCTTCAGATATGGTTCGAAA 1176
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Db 1040 TGGYCTGGGRTKAGGAGGAGGAGGAGGAGATGTTTTAAATGTTTMAAAAAAAYAA 1099
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QY 1177 AAAAAAAYAAAAA 1192
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Db 1100 AAAAAAAYAAAAA 1115
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RESULT 3
BM924140
LOCUS
DEFINITION BM924140 961 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6630474 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760345
5', mRNA sequence.
ACCESSION BM924140
VERSION BM924140.1 GI:19374507
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM12807 row: d column: 10
High quality sequence stop: 719.
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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5760345"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 74.3%; Score 886; DB 5; Length 961;
Best Local Similarity 98.8%; Pred. No. 4.8e-229;
Matches 908; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

263 AGTACCTCTTCTGAGGTACTTGGAAACCCACAGGCACACCCAGGCCCTCATCTTTGTGT 322
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Db 25 AGTACCTCTTCTGAGGTACTTGGAAACCCACAGGCACACCCAGGCCCTCATCTTTGTGT 84
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QY 323 CCCATGAGCGCGAGAGACAGTGGCGCTATGAAGAGTGGTCTCGGATGCTGATGGGCG 382
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QY 383 TGGACCTGCTGCTTTCGCCACACGACCATGTTGGCCACGGACAGACGAGCGAGGAGGA 442
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Db 145 TGGACCTGCTGCTTTCGCCACACGACCATGTTGGCCACGGACAGACGAGCGAGGAGGA 204
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QY 443 TGGTAGTGTCTGACTTTCACCGTTTTCGTCAGGGATGTTTTCAGCATGTGATTCATGTC 502
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QY 503 AGAAGACTACCTCGGGCTTCTGCTTCTTCTTCTGGGCACTCCATGGAGCGGCATCG 562
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Db 385 TGGTTCCTTGGCAATCTCTGAATCTGCAACAACTTTTCAAGGTCTTTCGTCGGAAGTCTCA 444
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QY 683 ACCTTGCTGCGCAAACTTGTCTTCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATA 742
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Db 445 ACCTTGCTGCGCAAACTTGTCTTCTCGGGCCCATCGACTCCAGCGTGTCTCTCTCGGAATA 504
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QY 743 AGACAGAGGTGCAATTTATTAACCTCAGACCCCTGATCTGCGGGCAGGGCTGAAGTGT 802
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Db 505 AGACAGAGGTGCAATTTATTAACCTCAGACCCCTGATCTGCGGGCAGGGCTGAAGTGT 564
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QY 803 GTTTCGGCATCCAACCTGCTGAATGCCGTCTCAGCGGTGGAGCGGCCCTCCCGCAAGCTGA 862
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Db 565 GTTTCGGCATCCAACCTGCTGAATGCCGTCTCAGCGGTGGAGCGGCCCTCCCGCAAGCTGA 624
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Db 625 CTGTGCGCTTCTGCTGCTCAGGGCTCTGCGGATCGCGCTATGTGACAGCAAGAGGGGCT 684
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QY 923 ACCTGCTCATGGAGTTAGCCAGAGCCAGACACTCTCAAGATTTATCAAGGTGCT 982
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Db 685 ACCTGCTCATGGAGTTAGCCAGAGCCAGACACTCTCAAGATTTATCAAGGTGCT 744
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QY	983	ACCATGTTCTCCACAGGAGCTTCCTGAAGTCACCAACTCCGCTCTCCATGAATAACA	1042
Db	745	ACCATGTTCTCCACAGGAGCTTCCTGAAGTCACCAACTCCGCTCTCCATGAATAACA	804
QY	1043	TGTGGGTCTCTCAAAAGGACAGCCAGCGAGGAATCGCTGCCCAACCTCGAATGCATT-GG	1101
Db	805	TGTGGGTCTCTCAAAAGGACAGCCAGCGAGGAATCGCTGCCCAACCTCGAATGCATTGG	864
QY	1102	CCGTCGCCGGCTCATGTCTGGG-GGATGCGAGGAGGGGAGGCGAGATGGCTTCTC	1160
Db	865	NCGGTCGCCGGCTCATGTCTGGGNGATGCGANGCAGGGGAGGCGANAGATGGCTTCTC	924
QY	1161	AGATATGGCTTGCAAAAAA	1179
Db	925	ANATATGGCTTGCAAAAAA	943
RESULT 4			
LOCUS	BX396587		
DEFINITION	BX396587 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1019YD19 5-PRIME, mRNA sequence.		
ACCESSION	BX396587		
VERSION	BX396587.2	GI:46876432	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li W.B., Gruber C., Jessee J. and Pollayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On May 13, 2003 this sequence version replaced gi:30621008. Contact: Genoscope		
FEATURES	source		
source	Genoscope - Centre National de Sequencage 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2061.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?c=CS0D1019CBI00P1&c=2061.r. Location/Qualifiers 1..926 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1019YD19" /tissue_type="PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
ORIGIN			
Query Match	74.0%;	Score 882.6;	DB 5; Length 926;
Best Local Similarity	99.1%;	Pred. No. 3.9e-228;	
Matches 879;	Conservative	7; Mismatches 1;	Indels 0; Gaps 0;
QY	1	CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC	60
Db	40	CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC	99
QY	61	TTGGGGCCGCCAGATAGGGAGACAGCCGATTTCCCTGGTTCTGATTCCTCAGGCTGTC	120
Db	100	TTGGGGCCGCCAGATAGGGAGACAGCCGATTTCCCTGGTTCTGATTCCTCAGGCTGTC	159
QY	121	GTGGTTGTGGAATGCAAAAGCCAGCACATAATGGAAACAGGACCTTGAAGACCTTCCAGC	180

Db	160	GTGGTTGTGGAATGCAAAAGCCAGCACATAATGGAAACAGGACCTTGAAGACCTTCCAGC	219
QY	181	ATCCAGAGAAAGTTCCCCAGCGGACCCCGAGAGCATTCCTCTACCAGGACTCCCT	240
Db	220	ATCCAGAGAAAGTTCCCCAGCGGACCCCGAGAGCATTCCTCTACCAGGACTCCCT	279
QY	241	CACCTGGTCAATGACAGCGGACAGTACTCTTCTGAGGTTACTGGAACCCACAGGACACA	300
Db	280	CACCTGGTCAATGACAGCGGACAGTACTCTTCTGAGGTTACTGGAACCCACAGGACACA	339
QY	301	CCCAAGGCCCTCATCTTTGTGTCCTGAGCGGAGAGCACAGTGGCCGCTATGAAGAG	360
Db	340	CCCAAGGCCCTCATCTTTGTGTCCTGAGCGGAGAGCACAGTGGCCGCTATGAAGAG	399
QY	361	CTGGCTCGGATGCTGATGGGGCTGGACCTGTGTGTGTCGCCCGACCATGTTGGCCAC	420
Db	400	CTGGCTCGGATGCTGATGGGGCTGGACCTGTGTGTGTCGCCCGACCATGTTGGCCAC	459
QY	421	GGACAGCGGAGGGAGAGGATGGTAGTGTCTGACTTCCACGTTTTCGTCAGGATGTG	480
Db	460	GGACAGCGGAGGGAGAGGATGGTAGTGTCTGACTTCCACGTTTTCGTCAGGATGTG	519
QY	481	TTGCAGCATGTGGATTCCATGCAAAAAGACTACCTGGGGCTTCTGTCTTCTTCTGGGC	540
Db	520	TTGCAGCATGTGGATTCCATGCAAAAAGACTACCTGGGGCTTCTGTCTTCTTCTGGGC	579
QY	541	CATCTCCATGGAGCGCCATCGCCATCTCACGGCCGAGAGAGCGCGGCCCATCTGCC	600
Db	580	CATCTCCATGGAGCGCCATCGCCATCTCACGGCCGAGAGAGCGCGGCCCATCTGCC	639
QY	601	GGCATGTACTCATTTGGCCTCTGGTTCTTGGCCAATCTGNAATCTGNAACAACCTTCAAG	660
Db	640	GGCATGTACTCATTTGGCCTCTGGTTCTTGGCCAATCTGNAATCTGNAACAACCTTCAAG	699
QY	661	GTCCTTGTGCGAAAGTGCTCAACTTGTGTGTCGCAAACTTGTCTCCGCGGCCCATCGAC	720
Db	700	GTCCTTGTGCGAAAGTGCTCAACTTGTGTGTCGCAAACTTGTCTCCGCGGCCCATCGAC	759
QY	721	TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATATACTCAGACCCCTGATC	780
Db	760	TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATATACTCAGACCCCTGATC	819
QY	781	TGCCGCGCAGGCTGAAGTGTGCTTCGGCATCCAACTGCTGAATGCGTCTCACGGGTG	840
Db	820	TGCCGCGCAGGCTGAAGTGTGCTTCGGCATCCAACTGCTGAATGCGTCTCACGGGTG	879
QY	841	GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTCTGCTGCTCCAGGG	887
Db	880	GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTCTGCTGCTCARGG	926
RESULT 5			
LOCUS	BUI62994		
DEFINITION	AGENCOURT 8073593 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083408 5', mRNA sequence.		
ACCESSION	BUI62994		
VERSION	BUI62994.1	GI:22676946	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	1 (bases 1 to 1011)		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		


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Best Local Similarity 97.1%; Pred. No. 1.6e-222;
Matches 951; Conservative 0; Mismatches 21; Indels 7; Gaps 7;

QY 1 CCAGCCGAAAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTTCTCGTGCC 60
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Db 5 CCCAGCCGAAAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTTCTCGTGCC 64
   |||

QY 61 TTGGGGCGCCAGATAGGGAACAGCCCGATTTGCTGGTTCGATTTCTCAGGCTGTC 120
   |||
Db 65 TTGGGGCGCCAGATAGGGAACAGCCCGATTTGCTGGTTCGATTTCTCAGGCTGTC 124
   |||

QY 121 GTGGTGTGGGAATGCAACGCCAGCACATAATGGAACAGGACCTGGAAGACCTTCCAGC 180
   |||
Db 125 GTGGTGTGGGAATGCAACGCCAGCACATAATGGAACAGGACCTGGAAGACCTTCCAGC 184
   |||

QY 181 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACGAGACCTCCCT 240
   |||
Db 185 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACGAGACCTCCCT 244
   |||

QY 241 CACCTGGTCAATGCAGAGGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
   |||
Db 245 CACCTGGTCAATGCAGAGGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 304
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QY 301 CCCAAGGCCCTCATCTTTGTGTCCTAGCGAGGACAGTGGCGGCTATGAAGAG 360
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Db 305 CCCAAGGCCCTCATCTTTGTGTCCTAGCGAGGACAGTGGCGGCTATGAAGAG 364
   |||

QY 361 CTGGCTCGGATCTGATGGGCTGAGCTGCTGGTGTTCGCCACGACCATGTTGGCCAC 420
   |||
Db 365 CTGGCTCGGATCTGATGGGCTGAGCTGCTGGTGTTCGCCACGACCATGTTGGCCAC 424
   |||

QY 421 GGACAGAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCAGTTCGTCAGGAGTGTG 480
   |||
Db 425 GGACAGAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCAGTTCGTCAGGAGTGTG 484
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QY 481 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTCGGCTTCCTGTCTTCTCTGGGC 540
   |||
Db 485 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTCGGCTTCCTGTCTTCTCTGGGC 544
   |||

QY 541 CACTTCATGGGAGGCGCATCGCCATCTCAGCGCGCAGAGAGGCGGGCCACTTCGCC 600
   |||
Db 545 CACTTCATGGGAGGCGCATCGCCATCTCAGCGCGCAGAGAGGCGGGCCACTTCGCC 604
   |||

QY 601 GGCATGTTACTCATTTCCGCTCTGGTCTTGGCAATCTGCAATCTGCAACACTTTCAG 660
   |||
Db 605 GGCATGTTACTCATTTCCGCTCTGGTCTTGGCAATCTGCAATCTGCAACACTTTCAG 664
   |||

QY 661 GTCCTTGTGCGAAAGTCTCAACCTTGTGTGTCGCAAACTTTGTCCCTCGGGCCATCGAC 720
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Db 665 GTCCTTGTGCGAAAGTCTCAACCTTGTGTGTCGCAAACTTTGTCCCTCGGGCCATCGAC 724
   |||

QY 721 TCCAGCGTCTCTTCGGAATAAGACAGAGTTCGACATTTATATACTCAGACCCGCTGATC 780
   |||
Db 725 TCCAGCGTCTCTTCGGAAT-AGACAGAGTTCGACATTTATATACTCAGACCCGCTGATC 783
   |||

QY 781 TGCCGGGCGGCTGAAAGTGTCTTCGGCATCCAACTGCTGAATGCGCTCTCAC-GGGT 839
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Db 784 TGCCGGGCGGCTGAAAGTGTCTTCGCAATCCAACTGCTGAATGCGCTCTCACGGGGT 843
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QY 840 GGAGCGCG-CCCTCCCAAGTGTACTGT- GCCCTTTCCTGCTGCTCCAGGGCTCTGCCGAT 897
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Db 844 GGAGCGCGCCCTCCCCAAGCTGACTGTGGCCCTTCTGCTGCTCCAGGGCTCTGCCGAT 903
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QY 898 -CGCTATGTGACAGCAAGGGGCTTA-CTGTCTCATGGAGTTAGCCAG-AGCCAGGAC 954
   |||
Db 904 CCGCTATGGGACAGCAAGGGGCTTACCCGGCTCTTGGAGTTAGCCCAAGAGCCGGAA 963
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QY 955 AAGACTCTCAAGATTATG 973
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Db 964 AAGACTCTCAGGATTTTG 982
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BU501241
LOCUS          BU501241          912 bp      mRNA      linear      EST 12-SEP-2002
DEFINITION    AGENCOURT 8877702 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6337918
               5', mRNA sequence.
ACCESSION     BU501241
VERSION       BU501241.1 GI:22803436
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 912)
               NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE         Unpublished (1999)
JOURNAL       Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
COMMENT       Tissue Procurement: ATCC
               cDNA Library Preparation: Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LICM9530 row: e column: 23
               High quality sequence stop: 881.

FEATURES             Location/Qualifiers
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         /lab_host="DH10B (phage-resistant)"
         /clone_lib="NIH MGC 43"
         /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
         EcoRI; cDNA made by oligo-dT priming. Directionally
         cloned into EcoRI/XhoI sites using the following 5'
         adaptor: GGCACGAG(G). Library constructed by Ling Hong
         in the laboratory of Gerald M. Rubin (University of
         California, Berkeley) using ZAP-cDNA synthesis kit
         (Stratagene) and Superscript II RT (Life Technologies).
         Note: this is a NIH_MGC Library."

ORIGIN
```

```
Query Match      72.2%; Score 860.8; DB 5; Length 912;
Best Local Similarity 99.4%; Pred. No. 3.3e-222;
Matches 884; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 CCAGCCGAAAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTTCTCGTGCC 60
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Db 15 CCAGCCGAAAGGAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTTCTCGTGCC 74
   |||

QY 61 TTGGGGCGCCAGATAGGGAACAGCCCGATTTGCTGGTTCGATTTCTCAGGCTGTC 120
   |||
Db 75 TTGGGGCGCCAGATAGGGAACAGCCCGATTTGCTGGTTCGATTTCTCAGGCTGTC 134
   |||

QY 121 GTGTTTGTGAATGCAACGCCAGCACATAATGGAACAGGACCTGGAAGACCTTCCAGC 180
   |||
Db 135 GTGTTTGTGAATGCAACGCCAGCACATAATGGAACAGGACCTGGAAGACCTTCCAGC 194
   |||

QY 181 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACGAGACCTCCCT 240
   |||
Db 195 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACGAGACCTCCCT 254
   |||

QY 241 CACCTGGTCAATGCAGAGGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
   |||
Db 255 CACCTGGTCAATGCAGAGGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 314
   |||

QY 301 CCCAAGGCCCTCATCTTTGTGTCCTAGGAGCCGAGAGCACAGTGGCGGCTATGAAGAG 360
   |||
Db 315 CCCAAGGCCCTCATCTTTGTGTCCTAGGAGCCGAGAGCACAGTGGCGGCTATGAAGAG 374
   |||
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QY 361 CTGGCTCGGATGCTGATGGGGCTGACCTGCTGGTGTTCGGCCACGACATGTTGGCCAC 420
 Db 375 CTGGCTCGGATGCTGATGGGGCTGACCTGCTGGTGTTCGGCCACGACATGTTGGCCAC 434
 QY 421 GGACAGCGAAGGGAGGAGGATGTAGTGTCTGACTTCCAGGTTTTCGTGAGGATGTG 480
 Db 435 GGACAGCGAAGGGAGGAGGATGTAGTGTCTGACTTCCAGGTTTTCGTGAGGATGTG 494
 QY 481 TTGACGATGTGGATTCCATGACAGAAAGACTACCTCGGGCTTCCTGTCTTCTTCTGGGC 540
 Db 495 TTGACGATGTGGATTCCATGACAGAAAGACTACCTCGGGCTTCCTGTCTTCTTCTGGGC 554
 QY 541 CACTTCATGGAGGCGCCATCCCATCTCTACGGCGCGAGAGAGCCGGGCACTTCGCC 600
 Db 555 CACTTCATGGAGGCGCCATCCCATCTCTACGGCGCGAGAGAGCCGGGCACTTCGCC 614
 QY 601 GGCAATGTACTCATTTCCGCTCTGGTCTTCCCAATCTGCAATCTGCAACTTTCGAAG 660
 Db 615 GGCAATGTACTCATTTCCGCTCTGGTCTTCCCAATCTGCAATCTGCAACTTTCGAAG 674
 QY 661 GTCCCTTGTGCGAAAGTGTCTCAACCTTGTGTGCTGCCAAACTTGTCCCTCGGGCCCATCGAC 720
 Db 675 GTCCCTTGTGCGAAAGTGTCTCAACCTTGTGTGCTGCCAAACTTGTCCCTCGGGCCCATCGAC 734
 QY 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATACTCAGACCCCTGATC 780
 Db 735 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATACTCAGACCCCTGATC 794
 QY 781 TGCCGGGAGGCTCAAGGTGTCTTCCGCATCCCACTGCTGCAATCTGCAACTTTCGAAG 839
 Db 795 TGCCGGGAGGCTCAAGGTGTCTTCCGCATCCCACTGCTGCAATCTGCAACTTTCGAAG 854
 QY 840 GGAGCGCCCTCCGCCAAGCTGACTGT-GCCCTTCTGCTGCTCCAGGG 887
 Db 855 GGAGCGCCCTCCGCCAAGCTGACTGTGCGCCCTTCTGCTGCTCCAGGG 903

RESULT 8

BUS41422 848 bp mRNA linear EST 13-SEP-2002
 LOCUS AGENCOURT_10333378 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573101
 DEFINITION 5', mRNA sequence.

ACCESSION BUS41422
 VERSION BUS41422.1 GI:22851863
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 848)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP

AUTHORS

cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

TITLE

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

JOURNAL

Plate: L10M2766 row: e column: 05

COMMENT

High quality sequence stop: 729.

FEATURES

source

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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6573101"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.7%; Score 842.2; DB 5; Length 848;
 Best Local Similarity 99.5%; Pred. No. 3.6e-217;
 Matches 844; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 345 TGGCGCGTATGAAGAGCTGGCTCGCATGCTGATGGGGCTGACCTGCTGGTGTTCGCCCA 404
 Db 1 TGGCGCGTATGAAGAGCTGGCTCGCATGCTGATGGGGCTGACCTGCTGGTGTTCGCCCA 60
 QY 405 CGACCATGTTGGCCACGACAGAGCGAAAGGGAGAGATGTTAGTGTCTGACTTCCACGT 464
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 QY 465 TTTTGTGAGGATGTGTTGACGATGTGGATTTCATGACAGAAAGACTACCTGGGCTTCC 524
 Db 121 TTTTGTGAGGATGTGTTGACGATGTGGATTTCATGACAGAAAGACTACCTGGGCTTCC 180
 QY 525 TGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATCGCCATCTCAGCGCCGACAGAG 584
 Db 181 TGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATCGCCATCTCAGCGCCGACAGAG 240
 QY 585 GCGGGGCACTTTCGCGGCATGTGTTCTTTCGCTTCTGTTTCTTTCGCAATCTCGAATC 644
 Db 241 GCGGGGCACTTTCGCGGCATGTGTTCTTTCGCTTCTGTTTCTTTCGCAATCTCGAATC 300
 QY 645 TGCACAACTTTCAAGTCTTCTGCTGCAAGTCTCAACTTGTGCTGCCAACTTGTCTC 704
 Db 301 TGCACAACTTTCAAGTCTTCTGCTGCAAGTCTCAACTTGTGCTGCCAACTTGTCTC 360
 QY 705 CTTGCGGCCCATCGACTCCAGCGTCTCTCGGAATAAGACAGAGTTCGACATTTATAA 764
 Db 361 CTTGCGGCCCATCGACTCCAGCGTCTCTCGGAATAAGACAGAGTTCGACATTTATAA 420
 QY 765 CTCAGACCCCTCTGATCTGCGGGCAGGGCTGAAGTGTGCTTTCGGCATCCAACTTCTG 824
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 QY 825 TGCGGTCTCAGGGTGGAGCGCGCCCTCCCAAGCTGCTGTCCTTCTGCTGCTCCA 884
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 QY 885 GGGCTCTCGCGATCGCCTATGTGACAGCAAGGGCCCTACCTGCTCATGGAGTTAGCAA 944
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 QY 945 GAGCCAGGACAAAGACTCTCAAGATTTATGAAGTGTGCTTTCCTCCCAAGGAGCT 1004
 Db 601 GAGCCAGGACAAAGACTCTCAAGATTTATGAAGTGTGCTTTCCTCCCAAGGAGCT 660
 QY 1005 TCTGTGAAGTCAACCACTTCTGCTTTCATGAAATAAATGTTGGTGTCTCTCAAGGACAGC 1064
 Db 661 TCTGTGAAGTCAACCACTTCTGCTTTCATGAAATAAATGTTGGTGTCTCTCAAGGACAGC 720
 QY 1065 CAGGGCAGGAACTGCGTCCCGCCAGCCCTGAATGCAATGGCCGGTCCCGGCTCATGGTCTGG 1124
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 Db 841 AAAAAAAA 848


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RESULT 9
BQ691581
LOCUS
DEFINITION BQ691581 944 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8341900 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249076
5', mRNA sequence.
ACCESSION BQ691581
VERSION BQ691581.1 GI:21816897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2389 row: p column: 05
High quality sequence stop: 751.
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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Query Match 70.4%; Score 839.6; DB 5; Length 944;
Best Local Similarity 97.9%; Pred. No. 1.9e-216; Mismatches 15; Indels 4; Gaps 2;
Matches 872; Conservative 0;

QY 1 CCAGCCCCGAAAGGCGAGGCTGGGTGCGGGAAGAGGGCTCGAGAGTGCCTTCCTGCTGCC 60
DB 6 CCAGCCCCGAAAGGCGAGGCTGGGTGCGGGAAGAGGGCTCGAGAGTGCCTTCCTGCTGCC 65
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QY 121 GTGGTTGTGGAAATCAACAGCCAGCACATATGGAACAGAGACCTGAAGACCTTCCAGC 180
DB 126 GTGGTTGTGGAAATCAACAGCCAGCACATATGGAACAGAGACCTGAAGACCTTCCAGC 185
QY 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACAGGACCTCCCT 240
DB 186 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACAGGACCTCCCT 245
QY 241 CACCTGTTCAATGCAGAGGACGATACCTCTTCTGCAGGTACTGGAAACCCACAGGACACA 300
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DB 366 CTGGCTCGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACGACCATGTGGCCAC 425  
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DB 426 GGACAGAGCGAAGGGAGAGGATGTTAGTCTGTGACTTCCACGTTTTCGTCAGGATGTG 485  
QY 481 TTGCAGCATGTGGATTCATCGCAAGAAAGACTACCTGGGCTTCCTGCTTCCTTCGGGC 540  
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QY 661 GTCCTTCTCGAAAGTGTCAACTTGTGTGCTGCCAAACTTGTCCCTCGGGCCCATCGAC 720  
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QY 781 TGCGGGCAGGGCTGAGAGTGTCTTCGGCATCCAACTGCTGAATGCTCTACAGGGTG 840  
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QY 841 GAGCGCG-CCCTCCCAAGCTGACTGTG-CCCTTCCTGCTGTCCAGGG 887  
DB 846 TGGAGCGCGCCCTCCCAAGCTGACTGTGCGCCCTTCCTGCTCTCCAANG 896
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RESULT 10
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LOCUS
DEFINITION BQ691355 896 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8340818 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249249
5', mRNA sequence.
ACCESSION BQ691355
VERSION BQ691355.1 GI:21816671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 896)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2390 row: g column: 10
High quality sequence stop: 745.
Location/Qualifiers
1..896
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6249249"

/tissue_type="ductal carcinoma, cell line"
/lab_host="DHI0B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match		67.3%;	Score 802.6;	DB 5;	Length 896;
Best Local Similarity		98.8%;	Pred. No. 2.1e-206;		
Matches 819;		Conservative 0;	Mismatches 9;	Indels 1;	Gaps 1;
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Qy	61	TTGGGGCCGCGCAGATGAGGAAACAGCCCGATTTGCCCTGTTCTGATTTCTCCAGSGTGC	120		
Db	65	TTGGGGCCGCGCAGATGAGGAAACAGCCCGATTTGCCCTGTTCTGATTTCTCCAGSGTGC	124		
Qy	121	GTGGTTGTGGAATCAACCGCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC	180		
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Qy	181	ATGCCAGGAAAGTTCCCGCAGGACCCCGAGAGCATTCCTTACGAGACTCCCT	240		
Db	185	ATGCCAGGAAAGTTCCCGCAGGACCCCGAGAGCATTCCTTACGAGACTCCCT	244		
Qy	241	CACCTGGTCAATGACAGCGACAGTACCTCTTCTGACGTACTTGAACCCACAGGACACA	300		
Db	245	CACCTGGTCAATGACAGCGACAGTACCTCTTCTGACGTACTTGAACCCACAGGACACA	304		
Qy	301	CCCAGGCGCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCGCTATGAAGAG	360		
Db	305	CCCAGGCGCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCGCTATGAAGAG	364		
Qy	361	CTGGCTGGATGCTGATGGGCTGGACCTGCTGTTGTCGCCACAGACCATGTTGGCCAC	420		
Db	365	CTGGCTGGATGCTGATGGGCTGGACCTGCTGTTGTCGCCACAGACCATGTTGGCCAC	424		
Qy	421	GGACAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTCCAGGATGTG	480		
Db	425	GGACAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTCCAGGATGTG	484		
Qy	481	TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCTGTTCTTCTTCTGGC	540		
Db	485	TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCTGTTCTTCTTCTGGC	544		
Qy	541	CATCTCATGGAGGGCCATCGCATCTCTACGGCGCGAGAGAGCGCGGCCACTTGGCC	600		
Db	545	CATCTCATGGAGGGCCATCGCATCTCTACGGCGCGAGAGAGCGCGGCCACTTGGCC	604		
Qy	601	GGCATGTACTCATTTGCGCTCTGTTCTTCCCAATCTGCAATCTGCAACAACTTTCAAG	660		
Db	605	GGCATGTACTCATTTGCGCTCTGTTCTTCCCAATCTGCAATCTGCAACAACTTTCAAG	664		
Qy	661	GTCTTGTGCGAAAGTCTCAACTTGTGTCGCAAACTTGTCCCTCGGGCCCATCGAC	720		
Db	665	GTCTTGTGCGAAAGTCTCAACTTGTGTCGCAAACTTGTCCCTCGGGCCCATCGAC	724		
Qy	721	TCCAGCGTCTCTCTCGGAATAAGACAGAGTTCACATTTATATACAGACCCCTGATC	780		
Db	725	TCCAGCGTCTCTCTCGGAATAAGACAGAGTTCACATTTATATACAGACCCCTGATC	784		
Qy	781	TGCCGGGCGAGGGCTG-AAGGTGCTTCCGGCATCCAACTGCTGAATGCC	828		
Db	785	TGCCGGGCGAGGGCTGAAAGGTGTCGTCGGCATCCAACTGCTGAATGCC	833		

RESULT 11

CN643629
LOCUS
DEFINITION
ILLUMIGEN MQO_8210 Katze MMR Macaca mulatta cDNA clone IBIUW:3354
5' similar to Bases 1 to 814 highly similar to human MGLL
(Hs.409826), mRNA sequence.
CN643629
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (bases 1 to 815)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2004.01.05. 794 Q20 bases.
PCR Primers
FORWARD: CCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGCGGATTTGGTA
Insert Length: 815 Std Error: 0.00
Plate: CL000097 row: C column: 03
Seq primer: CCTCACTAAAGGGAACAAAA
POLYA=Yes.

FEATURES

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/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:3354"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Eco I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN

Query Match		66.1%;	Score 788.4;	DB 7;	Length 815;
Best Local Similarity		98.0%;	Pred. No. 1.4e-202;		
Matches 798;		Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;
Qy	376	ATGGGGCTGGACCTGCTGGTGTTCGCCACGACCATTTGGCCACGACGAGCGAAGGG	435		
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Qy	436	GAGAGGATGTAGTGTCTGACTTCCAGTTTTCGTACGGATGTGTTGCAGCATGTGGAT	495		
Db	61	GAGAGGATGTAGTGTCTGACTTCCAGTTTTCGTACAGATGTGTTGCAGCATGTGGAT	120		
Qy	496	TCCATGCAGAAAGACTACCTCGGCTTCTCTGTTCTTCTTGGGCCACTCCATGGGAGGC	555		
Db	121	TCCATGCAGAAAGACTACCTCGGCTTCTCTGTTCTTCTTCTGGGCCACTCCATGGGAGGT	180		
Qy	556	GCCATGCCATCTCTACGGCGCAGAGAGCGCGGCCACTTTCGCCGCGATGGTACTATT	615		
Db	181	GCCATGCCATCTCTACGGCGCAGAGAGCGCGGCCACTTTCGCCGCGATGGTACTATT	240		
Qy	616	TCGGCTCTGGTCTTTCGCAATCTCGAATCTGCAACAACATTTCAAGGTCTTCTGCGGAAA	675		
Db	241	TCACCTCTGGTCTTTCGCAATCTCGAATCTGCAACAACATTTCAAGGTCTTCTGCGGAAA	300		

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Qy 676 GTGCTCAACCTGTGCTGCCAACTTGTCTCCCTCGGGCCATCGACTCCAGCGTCTCTCT 735
Db 301 GTGCTCAACCTGTGCTGCCAACTTGTCTCCCTCGGGCCATCGACTCCAGCGTCTCTCT 360
Qy 736 CGGAATAAGACAGAGGTGCGACATTTATACTCAGACCCCTCGATCTGCGGGCAGGGGTG 795
Db 361 CGGAATAAGACAGAGGTGCGACATTTATACTCAGACCCCTCGATCTGCGGGCAGGGGTG 420
Qy 796 AAGGTGTGCTTGGGCATCCAACTGCTGAATCCCTCTCACGGGTGGAGCGCCCTCCCC 855
Db 421 AAGGTGTGCTTGGGCATCCAGCTGCTGAATCCCTCTCACGGGTGGAGCGCCCTCCCC 480
Qy 856 AAGCTGACTGCGCCCTTCTGCTGCTCCAGGCTCTGCGGATCGCTATGTGACAGCAAA 915
Db 481 AAGCTGAGCGGTGCGCCCTTCTGCTGCTCCAGGCTCTGCGGATCGCTATGTGACAGCAAA 540
Qy 916 GGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACAGACTCTCAAGATTTATGAA 975
Db 541 GGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACAGACTCTCAAGATTTATGAA 600
Qy 976 GGTGCTACCATGTTCTCCAAAGAGCTTCTGAAAGTCAACAACTCGGTCTTCCATGAA 1035
Db 601 GGTGCTACCATGTTCTCCAAAGAGCTTCTGAAAGTCAACAACTCGGTCTTCCATGAA 660
Qy 1036 ATAACATGTGGGTCTCTCAAGACAGCCAGGACAGACTCGTCCCAACCTGATG 1095
Db 661 ATAACATGTGGGTCTCTCAAGACAGCCAGGACAGACTCGTCCCAACCTGATG 720
Qy 1096 CATTTGGCGGTGCGCGGCTCATGTCTTGGGGATGTCAGGAGGGGAGGAGATGGC 1155
Db 721 CACTGGCGGTGCGCGGCTCATGTCTTGGGGATGTCAGGAGGGGAGGAGATGGC 780
Qy 1156 TTCTCAGATGCGTTCGCAAAAAA 1189
Db 781 TTCTCAGATGCGTTCGCAAAAAA 814
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RESULT 12
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LOCUS BQ686359 878 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8064425 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206212
5', mRNA sequence.
ACCESSION BQ686359
VERSION BQ686359.1 GI:21811675
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM2360 row: f column: 05
High quality sequence stop: 667.
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/db_xref="caxon:9606"
/clone="IMAGE:6206212"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="caxon:9606"
/clone="IMAGE:6206212"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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RESULT 13

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/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 65.7%; Score 783.4; DB 5; Length 878;
Best Local Similarity 99.0%; Pred. No. 3.3e-201;
Matches 798; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 158 CAGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCCAGCGGACCCCGAGA 217
Db 72 CCGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCCAGCGGACCCCGAGA 131
Qy 218 GCATTCCCTACCAAGGACCTCCCTCAGCTGCTCAATGCAGACGGACACTTCTTCTGCA 277
Db 132 GCATTCCCTACCAAGGACCTCCCTCAGCTGCTCAATGCAGACGGACACTTCTTCTGCA 191
Qy 278 GGTACTGGAACCCACAGGCACACCCAAAGGCCCTCATCTTTGTGTCCTATGGAGCCGAG 337
Db 192 GGTACTGGAACCCACAGGCACACCCAAAGGCCCTCATCTTTGTGCCATGGAGCCGAG 251
Qy 338 AGCACAGTGGCGGTATGAAGAGCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGT 397
Db 252 AGCACAGTGGCGGTATGAAGAGCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGT 311
Qy 398 TCGCCACAGACCATGTTGGCCAGGACAGAGCGGAGGAGGAGATGCTAGTGTCTGACT 457
Db 312 TCGCCACAGACCATGTTGGCCAGGACAGAGCGGAGGAGGAGATGCTAGTGTCTGACT 371
Qy 458 TCCACGTTTTTCGTGAGGGATGTTGTCAGCATGTGGATTCCATGCAGAAAGACTACCCCTG 517
Db 372 TCCACGTTTTTCGTGAGGGATGTTGTCAGCATGTGGATTCCATGCAGAAAGACTACCCCTG 431
Qy 518 GGCTTCCTGCTTCTTCTGGGCACATCCATGGAGGGCCATCGCCATCTCAGGCGG 577
Db 432 GGCTTCCTGCTTCTTCTGGGCACATCCATGGAGGGCCATCGCCATCTCAGGCGG 491
Qy 578 CAGAGGCGCGGCGCACCTTCGCGGCATGTACTCATTTTCGCCCTCTGTTCTTCCCAATC 637
Db 492 CAGAGGCGCGGCGCACCTTCGCGGCATGTACTCATTTTCGCCCTCTGTTCTTCCCAATC 551
Qy 638 CTGAATCTGCAACAACTTCAAGGTCTTGTGTCGAAAGTCTCAACCTTGTGTGTCGCA 697
Db 552 CTGAATCTGCAACAACTTCAAGGTCTTGTGTCGAAAGTCTCAACCTTGTGTGTCGCA 611
Qy 698 ACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCA 757
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Qy 758 TTTATAACTCAGACCCCTCTGATCTGCGGGCAGGCGCTGAAGTGTGTTTCGGCATCCAAC 817
Db 672 TTTATAACTCAGACCCCTCTGATCTGCGGGCAGGCGCTGAAGTGTGTTTCGGCATCCAAC 731
Qy 818 TGCTGAATGCGGTCTCAAGGCTGAGGCGCCCTCCCAAGCTGACTGTGCTTCTTCTGTC 877
Db 732 TGCTGAATGCGGTCTCAAGGCTGAGGCGCCCTCCCAAGCTGACTGTGCTTCTTCTGTC 791
Qy 878 TGCTCAGGGCTCTGCGCATGCGCTATGTGACAGCAAGGGGCTTACTGCTCATGGAT 937
Db 792 TGCTCAGGGCTCTGCGCATGCGCTATGTGACAGCAAGGGGCTTACTGCTCATGGAT 851
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LOCUS      AGNCOURT_8071275 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090727
DEFINITION      5', mRNA sequence.
ACCESSION      BUI45364
VERSION      BUI45364.1 GI:22658896
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DFP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM2332 row: j column: 08
High quality sequence stop: 674.
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    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
    into EcoRI/XhoI sites using the following 5' adaptor:
    GGCACGAG(G). Library constructed by Ling Hong in the
    laboratory of Gerald M. Rubin (University of California,
    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
    Superscript II RT (Life Technologies). Note: this is a
    NIH_MGC Library."
ORIGIN
Query Match      64.8%; Score 772.2; DB 5; Length 916;
Best Local Similarity 96.8%; Pred. No. 3.7e-198;
Matches 798; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 158 CAGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCGCGGACCCCGCAGA 217
DB 77 CCGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCGCGGACCCCGCAGA 136

QY 218 GCATTCCCTACGAGACCTCCCTCACCTGGTCAATGACAGCGAGACGATACCTTCTGCA 277
DB 137 GCATTCCCTACGAGACCTCCCTCACCTGGTCAATGACAGCGAGACGATACCTTCTGCA 196

QY 278 GGTACTGGAACCCACAGGCACACCCAGGCCCTCATCTTTGTGTCCATGAGCGCGAG 337
DB 197 GGTACTGGAACCCACAGGCACACCCAGGCCCTCATCTTTGTGTCCATGAGCGCGAG 256

QY 338 AGCACAGTGGCCGTATGAAGAGTGGCTCCGATGCTGATGGGCTGACCTGCTGGTGT 397
DB 257 AGCACAGTGGCCGTATGAAGAGTGGCTCCGATGCTGATGGGCTGACCTGCTGGTGT 316

QY 398 TCGCCACGACCATGTTGGCCACGACAGCGAGCGAAGGGGAGAGGATGTTAGTGTGACT 457
DB 317 TCGCCACGACCATGTTGGCCACGACAGCGAGCGAAGGGGAGAGGATGTTAGTGTGACT 376

QY 458 TCCAGGTTTTCGTAGGAGATGTTTGCAGCATGTGGATTCATGACGAGAAAGACTACCTGT 517
DB 377 TCCAGGTTTTCGTAGGAGATGTTTGCAGCATGTGGATTCATGACGAGAAAGACTACCTGT 436

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QY 518 GGCTTCCTGCTCTTCTTCTGGGCATCTCCATGGAGCGGCATCGCCATCCTCTCAGGCGG 577
DB 437 GGCTTCCTGCTCTTCTTCTGGGCATCTCCATGGAGCGGCATCGCCATCCTCTCAGGCGG 496

QY 578 CAGAGAGCGCGGCGCACTTCCCGGCGATGCTACTCATTTGCGCCTTGGTTCTTGGCAATC 637
DB 497 CAGAGAGCGCGGCGCAGTTTCCCGGCGATGCTACTCATTTGCGCCTTGGTTCTTGGCAATC 556

QY 638 CTGAATCTGCAACAACATTTTCAAGGTCTTGTGCGAAAGTGTCAAACCTTGTGTGTCGCAA 697
DB 557 CTGAATCTGCAACAACATTTTCAAGGTCTTGTGCGAAAGTGTCAAACCTTGTGTGTCGCAA 616

QY 698 ACTTGTCCCTCGGCGCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCGACA 757
DB 617 ACTTGTCCCTCGGCGCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCGACA 676

QY 758 TTTATAACTCAGACCCCTCATCTGCGGCGAGGCTGAAGTGTGCTTCGGCATCCCAAC 817
DB 677 TTTATAACTCAGACCCCTCATCTGCGGCGAGGCTGAAGTGTGCTTCGGCATCCCAAC 736

QY 818 TGCTGAATGCGCTCTCACGGGTGGAGCGCGCTTCCCAAGCTGACTGTGCTTCTCTGTCG 877
DB 737 TGCTGAATGCGCTCTCACGGGTGGAGCGCGCTTCCCAAGCTGACTGTGCTTCTCTGTCG 796

QY 878 TGCTCCAGGCTCTGCGCATCGCTATGTGACAGCAAGGGGCTACTGCTCATGGAGT 937
DB 797 TGCTCCAGGCTCTGCGCATCGCTATGTGACAGCAAGGGGCTACTGCTCATGGAGG 856

QY 938 TAGCC--AAGAGCCAGGACCAAGACTCTCAAGATTATGAAGGTG 979
DB 857 GTACCGNAGAACCCAGAGGGGAGCTCTCAGGGATTATGAAGGTG 900

RESULT 14
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LOCUS      603023793F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194462 5',
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ACCESSION      BUI58109
VERSION      BUI58109.1 GI:15749687
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 806)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM11486 row: i column: 23
High quality sequence stop: 804.
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    /clone_lib="NIH_MGC_114"
    /note="Organ: bTain; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
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    primed and directionally cloned (EcoRV site is destroyed
    upon cloning). Average insert size 1.5 kb, insert size

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range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

Query Match 64.5%; Score 768.8; DB 4; Length 806;									
Best Local Similarity 99.4%; Pred. No. 3e-197;									
Matches 803; Conservative 0; Mismatches 2; Indels 3; Gaps 3;									
QY	282	CTGGAACCCACAGGCACACCAAGGCCCTCATCTTTGTGCCATGGAGCGGAGACGA	341						
Db	1	CTGGAACCCACAGGCACACCAAGGCCCTCATCTTTGTGCCATGGAGCGGAGACGA	60						
QY	342	CAGTGGCCGCTATGAGAGCTGGCTCGGATGCTGATGGGGTGGACCTGCTGGTTCGC	401						
Db	61	CAGTGGCCGCTATGAGAGCTGGCTCGGATGCTGATGGGGTGGACCTGCTGGTTCGC	120						
QY	402	CCACGACCATGTGGCCACAGACAGAGCGAAGGGGAGAGGATGTAGTCTGACTTCCA	461						
Db	121	CCACGACCATGTGGCCACAGACAGAGCGAAGGGGAGAGGATGTAGTCTGACTTCCA	180						
QY	462	CGTTTTCGTGAGGATGTGTCGACATGTGGATTCCATGCAGAAAGACTACCCCTGGGCT	521						
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QY	522	TCCTGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATCGCCATCTTCAGGGCGGAGA	581						
Db	241	TCCTGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATCGCCATCTTCAGGGCGGAGA	300						
QY	582	GAGGCGGGGCACATTCGCGGCATGGTACTATTTTCGCTCTGTTTTCGCAATCTCTGA	641						
Db	301	GAGGCGGGGCACATTCGCGGCATGGTACTATTTTCGCTCTGTTTTCGCAATCTCTGA	360						
QY	642	ATCTGCAACAACTTTCAAGGTCCTTGTGCGAAAGTGTCTCAACCTTGTGCTGCCAACTT	701						
Db	361	ATCTGCAACAACTTTCAAGGTCCTTGTGCGAAAGTGTCTCAACCTTGTGCTGCCAACTT	420						
QY	702	GTCCCTCGGGCCCATCGACTCGAGGTGCTCTCTCGGAATAAGACAGAGTTCGACATTTA	761						
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QY	762	TAACTCAGACCCCTGTATCTGCGGGCAGGCTGAAGTGTGCTTCGGCATCCCACTGCT	821						
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QY	822	GAATGCCGTCTCAGGGTGGAGCGGCCCTCCCCAAGCTGACTGTGCCCTTCTCTGCTGCT	881						
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QY	942	CAAGAGCCAGACAGACTCTCAAGATTTATGAGGTGCC-TACCATGTTCTCCACAGG	1000						
Db	660	CAAGAGCCAGACAGACTCTCAAGATTTATGAGGTGCC-TACCATGTTCTCCACAGG	719						
QY	1001	AGCTTCTGAAAGTACCAACTCCGTCCTTCCATGAAATAAATGTGGTCTCTCAAGGA	1060						
Db	720	AGCTTCTGAAAGTACCAACTCCGTCCTTCCATGAAAT-AACATGTGGTCTCTCAAGGA	778						
QY	1061	CAGCCACGGCAGAACTCGTCCCAACC	1088						
Db	779	CAGCCACGGCAGAACTCGTCCCAACC	806						
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DEFINITION									
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ACCESSION									
BU169041									
linear EST 04-SEP-2002									
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BU169041.1 GI:22683025
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2310 row: 1 column: 13
High quality sequence stop: 658.
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/organism="Homo sapiens"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match	64.2%;	Score 765.8;	DB 5;	Length 885;
Best Local Similarity	98.0%;	Pred. No. 2e-196;		
Matches 797;	Conservative 0;	Mismatches 12;	Indels 4;	Gaps 2;
Qy	158	CAGGACCTGAAGACCTTCCAGCATGCCAGAGGAAGTTCCTCCAGGCGGACCCCGCAGA	217	
Db	72	CCGGACCTGAAGACCTTCCAGCATGCCAGAGGAAGTTCCTCCAGGCGGACCCCGCAGA	131	
Qy	218	GCATTCCCTACCGAGGACCTCCCTCACCTGGTCAATGCAGACGGACAGTACCTCTTCTGCA	277	
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2	1192	100.0	1192	6	AX410763	Sequence
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5	1192	100.0	1573	9	BC006620	Homo sapi
6	1191	99.9	1192	9	BC000551	Homo sapi
7	1169.8	98.1	1890	9	AK091314	Homo sapi
8	1162	97.5	4193	6	AX281732	Sequence
9	937.2	78.6	942	9	CR456835	Homo sapi
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11	756.2	63.4	3863	10	MM0316580	Mus muscu
12	702	58.9	1316	10	BC057965	Mus muscu
13	701.8	58.9	3600	10	MM0011118	Mus muscu
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DEFINITION Sequence 3410 from Patent WO229103.
ACCESSION AX410763
VERSION AX410763.1 GI:21443468

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Alvares C., Horne D., Peres-da-Silva S. and Vockley J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3410 11-APR-2002;
GENE LOGIC INC (US)
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LOCUS Sequence 17 from Patent W002055705.
DEFINITION AX511610
ACCESSION AX511610
VERSION AX511610.1 GI:23392422
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Mezes,P.S., Rastelli,L., Hertmann,J.L., Macdougall,J.R., Zhong,H.,
Casman,S.J., Boldog,F., Shimkets,R.A., Gorman,L., Crasta,O.R.,
Mysoore,K.K., Folkerts,O., Martin,G.B., Eisen,A., Spaderna,S.K.,
Vernet,C.A., Bergh,C., Spytek,K.A., Dipippo,V.A., Zethusen,B.D.,
Peyman,J.A., Ellerman,K., Stone,D.J., Grosse,W.M., Alsobrook,J.P.,
Lepley,D.M., Rieger,D.K., Burgess,C.E. and Edinger,S.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 02055705-A 17 18-JUL-2002;
Curagen Corporation (US)
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Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
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DEFINITION Human lysophospholipase homolog (HU-K5) mRNA, complete cds.
ACCESSION U67963
VERSION U67963.1 GI:1763010
KEYWORDS
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REFERENCE
AUTHORS Upton,C. and Buller,R.M.L.
TITLE Human homolog of an ectromelia virus protein has similarity to
E.coli lysophospholipase
JOURNAL Unpublished
REFERENCE
AUTHORS Upton,C. and Buller,R.M.L.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-1996) Biochemistry and Microbiology, University
of Victoria, 150 Petch Building, Victoria, BC V8W 2Y2, Canada
REFERENCE
AUTHORS Wall,E.M., Cao,J., Chen,N., Buller,R.M. and Upton,C.
TITLE A novel poxvirus gene and its human homolog are similar to an E.
coli lysophospholipase
JOURNAL Virus Res. 52 (2), 157-167 (1997)
PUBMED 98154919
PUBMED 9495531
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Best Local Similarity 100.0%; Pred. No. 7e-276;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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IMAGE:3945191), complete cds.
ACCESSION BC006230
VERSION BC006230.2 GI:38197481
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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1 (bases 1 to 1573)
 Krausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Buetow, K., Krzywicki, M.I., Skalska, U., Smallos, D.E.,
 Scherz, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

2 (bases 1 to 1573)
 Krausberg, R.
 Direct Submission
 Submitted (09-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Nov 6, 2003 this sequence version replaced gi:13623260.
 Contact: MGC help desk
 Email: scapre-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 15 Row: b Column: 3
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 20127515.

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ORIGIN

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Best Local Similarity	100.0%	Pred. No. 6.9e-276		
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ACCESSION	BC000551		
VERSION	BC000551.2 GI:33988535		
KEYWORDS	MGC.		
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AUTHORS	1 (bases 1 to 1192)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1192)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Aug 20, 2003 this sequence version replaced gi:12653554. Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: c Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127515			
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DEFINITION	Sequence 141 from Patent WO0177389.		
ACCESSION	AX281732		
VERSION	AX281732.1	GI:16608983	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J., Mikita,T. and Tai,J.		
TITLE	Genes expressed in foam cell differentiation		
JOURNAL	Patent: WO 0177389-A 141 18-OCT-2001;		
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Db	752	ACCCAAGGCCCT	CATCTTTGTGTGCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGA 811
Qy	360	GCTGGCTCG	GAATGTGATGGGGCTGGACCTGTGCTGGTGTTCGCCACGACCATGTTGGCCA 419
Db	812	GCTGGCTCG	GAATGTGATGGGGCTGGACCTGTGCTGGTGTTCGCCACGACCATGTTGGCCA 871
Qy	420	CGGACAGCG	GAAGGGGAGAGGATGGTAGTCTGACCTCCACGCTTTTCGTGAGGATGT 479
Db	872	CGGACAGCG	GAAGGGGAGAGGATGGTAGTCTGACCTCCACGCTTTTCGTGAGGATGT 931
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Qy 540 CCACCTCCATGGAGCGCCATCGGCATCCTCACGGCGCAGAGAGCGCGGCACATTCGC 599
Db 992 CCACCTCCATGGAGCGCCATCGGCATCCTCACGGCGCAGAGAGCGCGGCACATTCGC 1051
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Qy 660 GGTCTCTGCTCGAAGTGCTCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
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Qy 720 CTCAGCGTGTCTCTCGAATAAGACAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 779
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Qy 780 CTGCGGGCAGCGGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
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Qy 1020 CTCGCTCTTCATGAATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1079
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Qy 1140 GAAGGCGCAGAGATGCTTCTCAGATATGCTTTC 1173
Db 1592 GAAGGCGCAGAGATGCTTCTCAGATATGCTTTC 1625

RESULT 9
CR456835
LOCUS Homo sapiens full open reading frame cDNA clone RZPD0834H044D for 942 bp mRNA linear PRI 03-JUN-2004
DEFINITION gene MGLL, monoglyceride lipase; complete cds, incl. stopcodon.
ACCESSION CR456835
VERSION CR456835.1 GI:48145786
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS Ebert,L., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 942)
AUTHORS Ebert,L., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE Direct Submision
JOURNAL Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT RZPD; RZPD0834H044D, ORFNO 1080
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834H044D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
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834 www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full length
expression clones generated by RZPD.
This CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC (ATG).
The last base of the last coding triplet has been changed to T,
which might lead to an amino acid change at the C terminus of the
polypeptide.
The stop codon has been set to TAA followed by
TTAACCCAGCTTCTT. att. Compared to the reference sequence NM_007283
we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
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Best Local Similarity 99.7%; Pred. No. 1.4e-214;
Matches 939; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 ATGGAACAGAGCCTGAAGACCTTCCAGCATGCCAGAGAAAGTCCCCAGCGGAC 60
Qy 211 CCGCAGAGCATTCCTACAGGACCTCCCTCACCTGCTCAATGCAGACGACGACCTC 270
Db 61 CCGCAGAGCATTCCTACAGGACCTCCCTCACCTGCTCAATGCAGACGACGACCTC 120
Qy 271 TTCTGAGGTACTGGAACCCACAGGACACCCAGGACCTCATCTTTGTGTCCATGGA 330
Db 121 TTCTGAGGTACTGGAACCCACAGGACACCCAGGACCTCATCTTTGTGTCCATGGA 180
Qy 331 GCCCGAGACACAGTGGCGCTATGAGAGCTGGCTGGATGCTGTGAGGCTGACCTG 390
Db 181 GCCCGAGACACAGTGGCGCTATGAGAGCTGGCTGGATGCTGTGAGGCTGACCTG 240
Qy 391 CTGTGTGTTCCCGACGACCATGTTGGCCACGACAGCGAAGGGGAGAGGATGTTAGT 450
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Qy 451 TCTGACTTCCACGTTTTTCTGTCAGGATGTGTGTCAGCATGTGATTCATGTCAGAAAGAC 510
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FEATURES

source

gene

CDS

ORIGIN


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Db      661 GAGCGCGCCCTCCCAAGCTGACTGTGCGCCCTTCCTGCTGCCAGGGCTCTGCCGATCGC 720
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Db      781 CTCAGATTATTAAGAGTGCCCTACCATGTTCTCCCAAGAGAGCTTCCTGAAAGTCAACCAAC 840
Qy      1021 TCCGCTCTCCATGAATAAACATGTGGCTCTCTCAAGAGCAGCCACCGCAGGAAGTGGC 1080
Db      841 TCCGCTCTCCATGAATAAACATGTGGGTCTCTCAAGAGCAGCCACCGCAGGAAGTGGC 900
Qy      1081 TCCCCACCCCTGA 1092
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DEFINITION Mus musculus mRNA for monoglyceride lipase (Mgll gene), transcript
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ACCESSION AJ316580
VERSION   AJ316580.1  GI:15617371
KEYWORDS alternative splicing; Mgll gene; monoglyceride lipase.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1
AUTHORS   Karlsson,M., Contreras,J.A., Hellman,U., Tornqvist,H. and Holm,C.
TITLE     cDNA cloning, tissue distribution, and identification of the
catalytic triad of monoglyceride lipase. Evolutionary relationship
to esterases, lysophospholipases, and haloperoxidases
J. Biol. Chem. 272 (43), 27218-27223 (1997)
98001701
PUBMED   9341166
REFERENCE 2
AUTHORS   Karlsson,M., Reue,K., Xia,Y.R., Lusis,A.J., Langin,D., Tornqvist,H.
and Holm,C.
TITLE     Exon-intron organization and chromosomal localization of the mouse
monoglyceride lipase gene
Gene 272 (1-2), 11-18 (2001)
21363420
PUBMED   11470505
REFERENCE 3 (bases 1 to 912)
AUTHORS   Holm,C.
TITLE     Direct Submission
Submitted (15-AUG-1997) Holm C., Cell and Molecular Biology, Lund
University, P.O. Box 94, S-221 00 Lund, SWEDEN
Revised by [4]
REFERENCE 4 (bases 1 to 3863)
AUTHORS   Holm,C.
TITLE     Direct Submission
Submitted (12-SEP-2001) Holm C., Cell and Molecular Biology, Lund
University, P.O. Box 94, S-221 00 Lund, SWEDEN
Related sequence: AJ001118. (alternative 5'UTR).
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source
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5' UTR

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3'UTR

polyA_signal

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Best Local Similarity 81.7%; Pred. No. 4.8e-171;
Matches 922; Conservative 0; Mismatches 203; Indels 4; Gaps 4;
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Qy 91 -ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 149
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Qy 210 CCCGAGAGCATTCCTTACAGGAGCTCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
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Qy 330 AGCCGAGAGCAGCAGTGGCGCTATGAAGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
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Qy 690 GCTGCACAACTTGTCCCTCGCGGCCCATCGATCCAGCGTGTCTCTCGGAATAAGACAGA 749
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RESULT 12
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LOCUS Mus musculus monoglyceride lipase, mRNA (cDNA clone MGC:67945
DEFINITION IMAGE:4986023), complete cds.
ACCESSION BC057965
VERSION BC057965.1 GI:34786022
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1316)
Strausberg,R.L., Feingold,E.A., Grouse,I.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A.C., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 12477932
PUBMED
REFERENCE 2 (bases 1 to 1316)
AUTHORS Strausberg,R.
DIRECT SUBMISSION
TITLE Submitted (08-SEP-2003) National Institutes of Health, Mammalian
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REMARK COMMENT
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S.,
Dieterich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 123 Row: b Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 15638943.
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Qy 158 CAGGACTGAGACCTTCAGCATGCCAGGAAGTTCCTCCAGCGGACCCGCGAGA 217
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278 GGTACTGGAACCCACAGGCACACCCAGGCGCTCATCTTTGTGTGCCATGAGCGCGAG 337
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578 CAGAGAGCGGGCGACCTTCGCCGCGATGTTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCT 637
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
506 CAGAGAGCGCAACCTACTTTCTGGCATGTCCTGATTTTACCTCTGCTGCTGCTGCTGCTGCT 565
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
566 CGGAATCTGCATGACCTTTGAAGTCTCTTGTGCGCAAACTCTCAATTTTGTCTGCGCAA 625
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
626 ATATGACCTTGGGGCGCATTAAGTCCAGCGTGTCTCGGAACAAGTCGAGGTTGACC 685
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
758 TTTTAACTCAGACCCCTGATCTGCGGGGAGGCTGGAAGTGTGCTTGGGCATCCAAC 817
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
986 GGATAGCAGCAGCAGGAGCTGGGTGTCCACCCTGAACATGCTGGCGAGCAACAGCTCA 1045
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DEFINITION Rattus norvegicus monoglyceride lipase (Mgl2) mRNA, complete cds.
ACCESSION AY081195
VERSION AY081195.1 GI:19697885
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 912)
AUTHORS Dinh.T.P., Carpenter,D., Leslie,P.M., Freund,T.F., Katona,I.,
Senai,S.L., Kathuria,S. and Piomelli,D.
TITLE Brain monoglyceride lipase participating in endocannabinoid
inactivation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (16), 10819-10824 (2002)
PUBMED 12136125
REFERENCE 2 (bases 1 to 912)
AUTHORS Dinh.T.P. and Piomelli,D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Pharmacology, UC Irvine, 360 Med Surge II,
Irvine, CA 92697, USA
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VLAALKLNFPLNPSILGRIDSVLSRNKSEVDLYNSDPLI CHAGVKVCFGIQLNAVY
RVERAMPRLTLPFLQLQGSADRLCKSGAYLLMESSPSQDKTLQWYEGAYHVLHKELP
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```

ORIGIN

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Query Match 56.0%; Score 667.2; DB 10; Length 912;
Best Local Similarity 83.2%; Pred. No. 1.3e-149;
Matches 759; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
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1 ATGCTGAGGCAAGTTCACCCAGCGAACTCCACAGAACGTCCTCTACCAGGACCTTCCT 60
QY 241 CACCTGCTCAATGACAGCGACAGTACTCTTCTGCAGGCTACTCGAAACCCACAGGCACA 300
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QY 301 CCCAAGGCCCTCATCTTTGTGTCCATGGAGCCGAGACAGCAGTGGCCGCTATGAAGAG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 CCCAAGGCCCTCATCTTCTGTCCTCATGGAGCTGGGAAACACTGTGGCCGTTATGACGAG 180
QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACAGCACCATTGTTGGCCAC 420
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QY 421 GGACAGAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGGAATGTG 480
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241 GGGCAGAGCCAGGGAGAGAGATGTTGATCGACTTCCAGTTTGTGTCAGAGATTGTG 300
QY 481 TTGCAGCATGTGGATTCCATGCAAGAAAGACTACCTGGGCTTCTGCTCTCTCTGCGGC 540
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301 TTGCAGCAGCTGAACACCGTCCAGAGGACTACCCCGAGGTCCCGCTTCTCTCTCTGCGGC 360
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 23:49:38 ; Search time 669 Seconds
(without alignments)
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Title: U67963

Perfect score: 1192

Sequence: 1 CCAGCCGAAAGGAGGGTC.....CAAAAAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s:*

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4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1192	100.0	1192	6	ABK84407 Human CDN
3	1192	100.0	1192	6	ABN96912 Gene #341
4	1192	100.0	1192	6	ABE59530 Human cDN
5	1192	100.0	1192	13	ADR52880 Drug ther
6	1192	100.0	1582	13	ADR14672 Human NF-
7	1192	100.0	1582	13	ADP24423 PRO polyp
8	1191	99.9	1192	12	ADO39191 Human cDN
9	1167	97.9	1192	12	ADL56807 Human SEC
10	1162	97.5	4193	6	AAS94886 Human DNA
11	1096	91.9	1613	10	ADI21843 Novel hum
12	1002	84.1	1309	9	AD57495 Human enz
13	952	79.9	1403	10	ADI21842 Novel hum
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18	667.2	56.0	912	10	ADB53684 Primary r
19	609	51.1	791	12	ADL57003 SECX-rela
20	519.8	43.6	556	9	ACH42006 Human foe

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23	464.4	39.0	576	10	ADI21384	Adi21384 Novel hum
24	417	35.0	452	9	ACH45286	Ach45286 Human foe
25	364.8	30.6	425	9	ACH20621	Ach20621 Human adu
26	355.2	29.8	393	2	AAQ61398	Aaq61398 Human bra
27	306.4	25.7	463	9	ACH36295	Ach36295 Human end
28	249.8	21.0	364	6	ABN22310	Abn22310 Human ORF
29	213	17.9	807	12	ADK70414	Adk70414 Respirato
30	210.6	17.7	501	9	ACH23413	Ach23413 Human adu
31	204.2	17.1	376	6	ABE69356	Abe69356 Novel mur
32	200	16.8	243	6	ABQ60334	Abq60334 Human col
33	198.4	16.6	506	6	ABK62789	Abk62789 Rat seque
34	127	10.7	143	2	AAT25567	Aat25567 Human gen
35	116.2	9.7	837	8	ACA38573	Aca38573 Prokaryot
36	116.2	9.7	972	8	ACA40296	Aca40296 Prokaryot
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40	84.8	7.1	825	13	ADS49720	Ads49720 Bacterial
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42	84.8	7.1	903	8	ACA25198	Aca25198 Prokaryot
43	71.4	6.0	840	8	ACA39992	Aca39992 Prokaryot
44	70.8	5.9	810	8	ADA71291	Ada71291 Rice gene
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ALIGNMENTS

RESULT 1

ABL59515

ID ABL59515 standard; cDNA; 1192 BP.

AC ABL59515;

XX 16-JUL-2002 (first entry)

XX Human lysophospholipase homologue cDNA SEQ ID NO:15.

DE Human; lysophospholipase homologue; enzyme; tumour;

KW Lipid associated gene; lipid metabolism; lipid synthesis; gene; ss.

XX Homo sapiens.

XX WO200227028-A1.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-US030366.

XX 28-SEP-2000; 2000US-00676052.

PR (ATAI-) ATAIRGIN TECHNOLOGIES INC.

FA Skinner MK, Patton JL, Chaudhary J;

PI WPI; 2002-405056/43.

DR Identifying tumor characteristics in a tissue sample taken from a

XX patient, involves determining the copy number or expression level of

PT genes associated with lipid metabolism, synthesis or action.

PT Example 1; Page 74; 113pp; English.

PS The present invention describes a method for identifying tumour

CC characteristics, comprising measuring a copy number or expression level

CC of at least two genes associated with lipid metabolism, synthesis, or

CC action in cells from a patient tissue sample, and comparing the results

CC with a copy number or expression level of the genes in a normal cell.

CC Also described is an array of nucleic acid polymers immobilised on a

CC solid support, comprising a solid support, at least two different nucleic

CC acid polymers which are each specific for a different gene associated

CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention
XX

Seq Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;
Query Match 100.0%; Score 1192; DB 6; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
ABK84407
ID ABR84407 standard; cDNA; 1192 BP.

XX ABK84407;

XX AC AC

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #978.

Human; ss; granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; ARDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030821.

XX 03-OCT-2000; 2000US-0237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of
genes associated with granulocyte activation, which serves as diagnostic
markers that is useful for monitoring disease states and drug toxicity.

XX Claim 1; SEQ ID NO 978; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a

PT level of expression of two or more genes in a liver tissue sample.

PS Claim 1; SEQ ID NO 3410; 298pp; English.

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cyclostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences

SQ Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;

Query Match	100.0%	Score 1192;	DB 6;	Length 1192;
Best Local Similarity	100.0%	Pred. No. 0;		
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			Indels	0;
			Gaps	0;

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Db	481	TTGACGATGTGGATTTCCATGCAGAAAGACTACCTCGGGCTTCCTGTCTTCTCTTGGGC	540
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PA (CURA-) CURAGEN CORP.

XX Mezes PS, Rastelli L, Herimann JL, Macdougall JR, Zhong H;

PI Gaman SJ, Boldog F, Shinkets RA, Gorman L, Crasta OR, Mysoore KK;

PI Folkerts O, Martin GB, Eissen A, Spaderna SK, Vernet CAM, Bergh C;

PI Szytek KA, Dipippo VA, Zehrhusen BD, Feyman JA, Ellerman K, Stone DJ;

PI Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;

PI Edinger S;

XX WPI; 2002-590675/63.

DR P-PSDB; ABG76945.

XX Human SECK/NOVX polypeptide useful for diagnosing, preventing or treating

PT disorders associated with aberrant expression or activity of SECK/NOVX

PT nucleic acids and proteins e.g., diabetes.

XX Disclosure; Page 55; 443pp; English.

XX The invention discloses the isolated human polypeptides, and

CC polynucleotides encoding them, that have been designated SECK and NOVX.

CC The polypeptides can be used for treating, or delaying, the onset of an

CC angiogenic-associated disorder or treating a pathological state in a

CC subject, preferably a mammal. They can also be used in determining the

CC presence of, or predisposition to, a disease associated with altered

CC levels of the polypeptides and polynucleotides of any one of the 12

CC sequences (SECK-12), for raising antibodies, for identifying an agent

CC that binds to, or that modulates the expression or activity of the

CC polypeptide, for treating or preventing a NOVX-associated disorder (NOV1-

CC 8) and as a pharmaceutical composition comprising the polypeptide,

CC polynucleotide or the antibody. The polypeptides and polynucleotides are

CC useful in diagnostic applications where their amounts are assessed, or

CC for the manufacture of a medicament (e.g. gene therapy) for treating or

CC preventing disorders or syndromes such as developmental disorders, immune

CC diseases, signal transduction pathway disorders, metabolic disorders,

CC feeding disorders (including obesity), wasting disorders,

CC neurodegenerative disorders (including Alzheimer's disease and

CC Parkinson's disease), behavioural disorders, allergies, asthma,

CC atherosclerosis, cardiomyopathy, angina pectoris, autoimmune diseases,

CC retinal diseases, cirrhosis, diabetes, infectious disease (bacterial,

CC fungal, protozoal and viral e.g. human immunodeficiency virus, HIV),

CC cancer (e.g. prostate cancer), hypertension, hypotension, multiple

CC sclerosis, urinary retention, osteoporosis, Crohn's disease, ulcers,

CC neurological disorders (e.g. anxiety), haemophilia or cirrhosis. They may

CC also be used as immunogens to produce antibodies specific for the

CC invention, and as vaccines. Further, they are useful for screening

CC potential agonist and antagonist compounds. The sequences presented in

CC AB559522-AB559541 are the human SECK-12 and NOV1-8 cDNAs

XX

SQ Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;

Query Match 100.0%; Score 1192; DB 6; Length 1192;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCGAAAGGAGGCTTGGGTGCGGGAAGAGGGCTCGAGAGCTGCTTCTGCTGCC 60

Db 1 CCAGCCGAAAGGAGGCTTGGGTGCGGGAAGAGGGCTCGAGAGCTGCTTCTGCTGCC 60

Qy 61 TTGGGGCCCGCCAGATGAGGGAACAGCCCGATTTGCTGGTTCGTATCTCAGGCTGTC 120

Db 61 TTGGGGCCCGCCAGATGAGGGAACAGCCCGATTTGCTGGTTCGTATCTCAGGCTGTC 120

Qy 121 GTGGTTGTGGAAATGCAACCGCCAGCACATATATGAAACAGGACCTGAAGACCTTCCAGC 180

Db 121 GTGGTTGTGGAAATGCAACCGCCAGCACATATATGAAACAGGACCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACAGGACCTCCCT 240

Db 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACAGGACCTCCCT 240

Qy 241 CACCTGGTCAATGCGAGCGGACGATACCTCTTCTGCGAGGTAATGGAACCCACAGGCA 300

Db 241 CACCTGGTCAATGCGAGCGGACGATACCTCTTCTGCGAGGTAATGGAACCCACAGGCA 300

Qy 301 CCCAAGGCCCTCATCTTTTGTGTCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360

Db 301 CCCAAGGCCCTCATCTTTTGTGTCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360

Qy 361 CTGGCTCGATGCTGATGGGGCTGGACCTGTGTGTGTTCGCCACAGACCATGTTGGCCAC 420

Db 361 CTGGCTCGATGCTGATGGGGCTGGACCTGTGTGTGTTCGCCACAGACCATGTTGGCCAC 420

Qy 421 GGACAGAGCGAAGGGGAGAGGATGATGTCTACCTTCCACGTTTTCGTGAGGATG 480

Db 421 GGACAGAGCGAAGGGGAGAGGATGATGTCTACCTTCCACGTTTTCGTGAGGATG 480

Qy 481 TTGACGATGTTGATTCATGCGAAGAGACTACCTTGGGCTTCTCTTCTTCTGCGC 540

Db 481 TTGACGATGTTGATTCATGCGAAGAGACTACCTTGGGCTTCTCTTCTTCTGCGC 540

Qy 541 CACTCCATGGAGGGCGCATCGCCATCTCAGGCGCGAGAGCGCGGGCACTTTCGCC 600

Db 541 CACTCCATGGAGGGCGCATCGCCATCTCAGGCGCGAGAGCGCGGGCACTTTCGCC 600

Qy 601 GGCATGTACTCATTTTCGCTCTGTTTTCGCCAATCTGAATCTGCAACAACTTTCAAG 660

Db 601 GGCATGTACTCATTTTCGCTCTGTTTTCGCCAATCTGAATCTGCAACAACTTTCAAG 660

Qy 661 GTCCTTCTGCGAAGTGCTCAACTTGTGTGTGCGCAAACTTGTCTCGGCGCCATCGAC 720

Db 661 GTCCTTCTGCGAAGTGCTCAACTTGTGTGTGCGCAAACTTGTCTCGGCGCCATCGAC 720

Qy 721 TCCAGCGTCTCTCGGAATAAGACAGAGTGCACATTTATTAATCAGACCCCTGATC 780

Db 721 TCCAGCGTCTCTCGGAATAAGACAGAGTGCACATTTATTAATCAGACCCCTGATC 780

Qy 781 TCCGCGCAGGGCTGAAGGTGTCTCGGCATCCAACTGCTGAATGCCGTCTCAGGGTG 840

Db 781 TCCGCGCAGGGCTGAAGGTGTCTCGGCATCCAACTGCTGAATGCCGTCTCAGGGTG 840

Qy 841 GAGCGCCCTTCCCAAGCTGACTGTGCTTCTGCTGCTTCCAGGGCTCTGCGGATCGC 900

Db 841 GAGCGCCCTTCCCAAGCTGACTGTGCTTCTGCTGCTTCCAGGGCTCTGCGGATCGC 900

Qy 901 CTATGTGACAGAAAGGGGCTACCTGCTCATGAGTTAGCAAGAGCCAGGACAAGACT 960

Db 901 CTATGTGACAGAAAGGGGCTACCTGCTCATGAGTTAGCAAGAGCCAGGACAAGACT 960

Qy 961 CTCAGATTTATGAGGTGCTACCATGTTCTCCACAAGGAGTTCCTGAAGTCAACCAAC 1020

Db 961 CTCAGATTTATGAGGTGCTACCATGTTCTCCACAAGGAGTTCCTGAAGTCAACCAAC 1020

Qy 1021 TCCGCTTCTCCATGAATAAACAATGTGGTCTCTCAAGGAGCAGCCAGGCAAGTCCG 1080

Db 1021 TCCGCTTCTCCATGAATAAACAATGTGGTCTCTCAAGGAGCAGCCAGGCAAGTCCG 1080

Qy 1081 TCCCAACCTGAAATGCAATGCGCGGTGCCGGCTCATGTTCTGGGGATGACGAGGGG 1140

Db 1081 TCCCAACCTGAAATGCAATGCGCGGTGCCGGCTCATGTTCTGGGGATGACGAGGGG 1140

Qy 1141 AAGGGCAGAGATGCTTCTCAGATATGCTTGCATAAAAAAAAAAAAAAAAAAAAA 1192

Db 1141 AAGGGCAGAGATGCTTCTCAGATATGCTTGCATAAAAAAAAAAAAAAAAAAAAA 1192

RESULT 5

ADR52880

ID ADR52880 standard; DNA; 1192 BP.

XX ADR52880;

XX AC

XX DT 18-NOV-2004 (first entry)

XX DE Drug therapy altered expressed gene #231.

XX KW drug activity monitoring; expression profile; gene expression;

KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
KW mTOR; ds.
XX
OS Homo sapiens.
PN WO2004072265-A2.
XX
XX 26-AUG-2004.
PD
PF 11-FEB-2004; 2004WO-US004118.
XX
XX 11-FEB-2003; 2003US-0446133p.
PR 03-APR-2003; 2003US-0459782p.
PR 23-JAN-2004; 2004US-0538246p.
XX
XX (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TREP/) TREPICCHIO W L.
XX
XX Burczynski M, Twine N, Dornier AJ, Trepicchio WL;
PI WPI; 2004-642301/62.
XX
XX Disclosure; SEQ ID NO 231; 136pp; English.
XX
XX The invention relates to a method of monitoring drug activities in vivo
CC by comparing an expression profile of at least one gene in a peripheral
CC blood sample of a patient to a reference expression profile of the at
CC least one gene, where the at least one gene is differentially expressed
CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
CC blood disease and are subjected to a drug therapy as compared to PBMCs
CC isolated from the patient before the drug therapy, and where the patient
CC has the non-blood disease and is being treated by the drug therapy. The
CC method, kit, and nucleic acid array are useful for monitoring drug
CC activities in vivo. The drug is especially CCI-779, an ester analogue of
CC the immunosuppressant rapamycin (mTOR). This sequence represents a gene
CC mammalian target of rapamycin (mTOR). This sequence represents a gene
CC expressed in PBMC altered by the drug therapy. (Note: this sequence does
CC no form part of the printed specification but was obtained in electronic
CC format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
XX
XX Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1192; DB 13; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGCCCCAAGAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTCTCTGCTGCC 60
DB 1 CCAGCCCCAAGAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTCTCTGCTGCC 60
QY 61 TTGGGGCCGCCAGATGAGGAAACAGCCGATTTGCTGGTTCTGATTTCCAGGCTGTC 120
DB 61 TTGGGGCCGCCAGATGAGGAAACAGCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC 120
QY 121 GTGGTTGTGGATGCAACGCCAGCACATATGGAACAGGACCTGAGACCTTCCAGC 180
DB 121 GTGGTTGTGGATGCAACGCCAGCACATATGGAACAGGACCTGAGACCTTCCAGC 180
QY 181 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACCGAGACTCCCT 240
DB 181 ATGCCAGAGGAAGTTCCCCCAGGCGGACCCCGCAGAGCATTTCCCTACCGAGACTCCCT 240
QY 241 CACCTGTGTAATGACAGCGGACGATGCTCTTCTGCGAGGTCTGGAACCCACAGGACACA 300
DB 241 CACCTGTGTAATGACAGCGGACGATGCTCTTCTGCGAGGTCTGGAACCCACAGGACACA 300

QY 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCGCTATGAAGAG 360
DB 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCGCTATGAAGAG 360
QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTCGCCACGACACATGTTGGCCAC 420
DB 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTCGCCACGACACATGTTGGCCAC 420
QY 421 GGACAGAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480
DB 421 GGACAGAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480
QY 481 TTGCAGCATGTGGAATTCATGCAAGAAAGACTTACCTGGGCTTCTGCTGCTTCTTGGC 540
DB 481 TTGCAGCATGTGGAATTCATGCAAGAAAGACTTACCTGGGCTTCTGCTGCTTCTTGGC 540
QY 541 CACTCCATGGAGGCGGCATCGCCATCTCACGGCCGACAGAGGCGGGGCACTTTCGCC 600
DB 541 CACTCCATGGAGGCGGCATCGCCATCTCACGGCCGACAGAGGCGGGGCACTTTCGCC 600
QY 601 GGCATGTACTCATTTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 GGCATGTACTCATTTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GTCCCTTCTGCGAAGTGCTCAACCTTGTGCTGCCAACTTGTCCCTCGGGCCCATCGAC 720
DB 661 GTCCCTTCTGCGAAGTGCTCAACCTTGTGCTGCCAACTTGTCCCTCGGGCCCATCGAC 720
QY 721 TCCAGCGTGTCTCTCGAATAAGACAGAGGTGACATTTTATAACTCAGACCCCTGATC 780
DB 721 TCCAGCGTGTCTCTCGAATAAGACAGAGGTGACATTTTATAACTCAGACCCCTGATC 780
QY 781 TGCCGGCAGGCGTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCGCTCTCACGGGTG 840
DB 781 TGCCGGCAGGCGTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCGCTCTCACGGGTG 840
QY 841 GAGCGCGCTTCCCAAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 GAGCGCGCTTCCCAAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 CTATGTGACAGCAAGGGGCTTCTGCTCATGAGTTAGCCAAAGAGCAGGACAAGACT 960
DB 901 CTATGTGACAGCAAGGGGCTTCTGCTCATGAGTTAGCCAAAGAGCAGGACAAGACT 960
QY 961 CTCAGATTTATGAAGTGCTTCCATGTTCTCCAAAGGAGCTTCTGAAGTCAACCAAC 1020
DB 961 CTCAGATTTATGAAGTGCTTCCATGTTCTCCAAAGGAGCTTCTGAAGTCAACCAAC 1020
QY 1021 TCCGTCTTCCATGAATAAATCATGTGGTGTCTCAAAGGACAGCCAGGCAAGCACTGCG 1080
DB 1021 TCCGTCTTCCATGAATAAATCATGTGGTGTCTCAAAGGACAGCCAGGCAAGCACTGCG 1080
QY 1081 TCCCCACCTTGAATGCAATGCGTCCCGGCTCATGTTCTGGGGATGTCAGGAGGG 1140
DB 1081 TCCCCACCTTGAATGCAATGCGTCCCGGCTCATGTTCTGGGGATGTCAGGAGGG 1140
QY 1141 AAGGGCAGAGATGCGCTTCTCAGATATGGCTTGCAAAAAAAGGGGAGGGG 1192
DB 1141 AAGGGCAGAGATGCGCTTCTCAGATATGGCTTGCAAAAAAAGGGGAGGGG 1192

RESULT 6

ADRI4672

ID ADRI4672 standard; DNA; 1592 BP.

XX AC ADRI4672;

XX AC ADRI4672;

DT 21-OCT-2004 (first entry)

XX

DE Human NF-kappaB pathway-associated gene SeqID673.

XX

KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW	antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW	antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW	immunosuppressive; vulnerary; gene therapy; immune disorder;
KW	inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW	hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW	hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW	X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW	viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW	viral replication; host cell survival; evasion of immune response;
KW	rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW	atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW	autoimmune disorder; hyper immune activity;
KW	aberrant acute phase response; hypercongenital condition; birth defect;
KW	neurotic lesion; wound; organ transplant rejection;
KW	aberrant signal transduction; proliferating disorder; cancer;
KW	HIV propagation; gene; ds; human.
XX	
XX	Homo sapiens.
XX	
XX	WO2004065577-A2.
XX	
XX	05-AUG-2004.
XX	
XX	13-JAN-2004; 2004WO-US0000798.
XX	
XX	14-JAN-2003; 2003US-0440068P.
PR	
PR	12-MAY-2003; 2003US-0469757P.
XX	
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
XX	Nadler SG, Neubauer MG, Feder JN, Carman J;
PI	
XX	WPI; 2004-562168/54.
DR	
DR	P-PSDB; ADRI4673.
XX	
PT	New isolated polynucleotides and polypeptides associated with NF-kappaB
PT	pathway, useful for diagnosing, treating, or preventing disorders or
PT	diseases associated with NF-kappaB pathway.
XX	
XX	Claim 1; SEQ ID NO 673; 237pp; English.
PS	

Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CCAGCCGAAAGCAGGCTCTGGGTGCGGAAGAGGGCTCGAGCTGCCTTCTCTGTGCC 60
Db	379 CCAGCCGAAAGCAGGCTCTGGGTGCGGAAGAGGGCTCGAGCTGCCTTCTGTGTGCC 438
Qy	61 TTGGGGCGCCAGATGAGGAAACAGCCGATTTGCCTGTCTTCTGATTTCTCAGGCTGTC 120
Db	439 TTGGGGCGCCAGATGAGGAAACAGCCGATTTGCCTGTCTTCTGATTTCTCAGGCTGTC 498
Qy	121 GTGGTTCTGGAAATGCAAAACCCAGCACATAATATGAAACAGAGCTGTGAAGACCTTCCAGC 180
Db	499 GTGGTTCTGGAAATGCAAAACCCAGCACATAATATGAAACAGAGCTGTGAAGACCTTCCAGC 558
Qy	181 ATGCCAGAGAAAGTTTCCCCAGCGGACCCCGCAGAGCAATCCCTACCAAGGACCTCCCT 240
Db	559 ATGCCAGAGAAAGTTTCCCCAGCGGACCCCGCAGAGCAATCCCTACCAAGGACCTCCCT 618
Qy	241 CACTGTGTCAATGCAGACGACAGTAGTACTCTTCTGCAAGTACTTGGAAACCCACAGGCACA 300
Db	619 CACTGTGTCAATGCAGACGACAGTAGTACTCTTCTGCAAGTACTTGGAAACCCACAGGCACA 678
Qy	301 CCCAAGGCCCTCATCTTTGTGTCCTATGGAGCCGAGAGCACAGTGGCCGTATGAAGAG 360
Db	679 CCCAAGGCCCTCATCTTTGTGTCCTATGGAGCCGAGAGCACAGTGGCCGTATGAAGAG 738
Qy	361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGTGTTCCGCCACGACCAATGTTGGCCAC 420
Db	739 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGTGTTCCGCCACGACCAATGTTGGCCAC 798
Qy	421 GGAACAGAGCAAGGGGAGAGGATGGTAGTGTCTGTACTTCCACGTGTTTCGTACGGGATGTG 480
Db	799 GGAACAGAGCAAGGGGAGAGGATGGTAGTGTCTGTACTTCCACGTGTTTCGTACGGGATGTG 858
Qy	481 TTGCAGCATGTGGAATTCATGCGAAGAGACTACCTGGGGTTCCTGTCTTCTTCTTGGGC 540
Db	859 TTGCAGCATGTGGAATTCATGCGAAGAGACTACCTGGGGTTCCTGTCTTCTTCTTGGGC 918
Qy	541 CACTTCCATGGAGCGCCATCGCCATCCTCACGGCCGCGAGAGGGCGGGCCACTTTGCGCC 600
Db	919 CACTTCCATGGAGCGCCATCGCCATCCTCACGGCCGCGAGAGGGCGGGCCACTTTGCGCC 978
Qy	601 GGCATGTGATCTCATTTGCGCTCTGGTTCTTGGCCAAATCTCTGAATCTGCGAACAACTTTCAAG 660
Db	979 GGCATGTGATCTCATTTGCGCTCTGGTTCTTGGCCAAATCTCTGAATCTGCGAACAACTTTCAAG 1038
Qy	661 GTCTCTTCTCGGAAGTGCTCAACCTTGCTGCGCCAAACTTGTGTCCTCGGGGCCCATCGAC 720
Db	1039 GTCTCTTCTCGGAAGTGCTCAACCTTGCTGCGCCAAACTTGTGTCCTCGGGGCCCATCGAC 1098
Qy	721 TCAGCGTGCTCTCTCGAAATAAGACAGAGGTGCAATTTATAACTCAGACCCCTTGATC 780
Db	1099 TCAGCGTGCTCTCTCGAAATAAGACAGAGGTGCAATTTATAACTCAGACCCCTTGATC 1158
Qy	781 TGGCGGACAGGCTGAAGGTGTCTTCGGCATCCAATGCTGAATCGCGTCTCACGGGTG 840
Db	1159 TGGCGGACAGGCTGAAGGTGTCTTCGGCATCCAATGCTGAATCGCGTCTCACGGGTG 1218
Qy	841 GAGGGCGCCCTCCCAAGCTGACTGTGTGCCCTTCTGTGTCTCAGGGCTCTGCGCATCGC 900
Db	1219 GAGGGCGCCCTCCCAAGCTGACTGTGTGCCCTTCTGTGTCTCAGGGCTCTGCGCATCGC 1278
Qy	901 CTATGTGACAGCAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACAAGACT 960
Db	1279 CTATGTGACAGCAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACAAGACT 1338
Qy	961 CTCAGAATTTATGAAGGTGCTTACCATTGTTCTCCACAAGGAGCTTCTGTAAGTCAACAAC 1020
Db	1339 CTCAGAATTTATGAAGGTGCTTACCATTGTTCTCCACAAGGAGCTTCTGTAAGTCAACAAC 1398
Qy	1021 TCGGTCTTCCATGAATAAATCATGTGGTCTCTCAAAGGACAGCCACGGCAGGAACCTGGC 1080
Db	1399 TCGGTCTTCCATGAATAAATCATGTGGTCTCTCAAAGGACAGCCACGGCAGGAACCTGGC 1458

Db	1279	CTATGTGACAGCAAGGGCGCTTACCTGCTCATGTGAGTTAGCCAGAGCCAGCAAGACT	1338
QY	961	CTCAAGATTATGAAGGTGCGCTTACCATTGTTCTCCACAGGAGCTTCTCTGAAGTCAACCAAC	1020
Db	1339	CTCAAGATTATGAAGGTGCGCTTACCATTGTTCTCCACAGGAGCTTCTCTGAAGTCAACCAAC	1398
QY	1021	TCCGTCCTTCATGAATAAACAATGTGGGTCTCTCAAGAGACAGCCACGGCAGGAAGTCCG	1080
Db	1399	TCCGTCCTTCATGAATAAACAATGTGGGTCTCTCAAGAGACAGCCACGGCAGGAAGTCCG	1458
QY	1081	TCCCCACCTCAATGATGCGCGGTGCCGCTCATGCTCTGGGGATGCGAGCAGGGG	1140
Db	1459	TCCCCACCTCAATGATGCGCGGTGCCGCTCATGCTCTGGGGATGCGAGCAGGGG	1518
QY	1141	AAGGCGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAAAAA	1192
Db	1519	AAGGCGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAAAAA	1570
RESULT 8			
ADO39191	ID ADO39191 standard; cDNA; 1192 BP.		
XX	AC	ADO39191;	
XX	DT	15-JUL-2004 (first entry)	
XX	DE	Human cDNA encoding novel secreted protein SEC9.	
XX	KW	Human; ss; gene; secreted protein; SECX; cardiomyopathy; atherosclerosis;	
XX	KW	hypertension; congenital heart defect; aortic stenosis;	
XX	KW	atrial septal defect; atrioventricular canal defect; ductus arteriosus;	
XX	KW	pulmonary stenosis; subaortic stenosis; ventricular septal defect;	
XX	KW	valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;	
XX	KW	congenital adrenal hyperplasia; prostate cancer; neoplasm;	
XX	KW	adenocarcinoma; lymphoma; uterus cancer; haemophilia; hypercoagulation;	
XX	KW	idiopathic thrombocytopaenic purpura; immunodeficiency;	
XX	KW	graft versus host disease; AIDS; bronchial asthma; Crohn's disease;	
XX	KW	multiple sclerosis; angiogenic-associated disorder; psoriasis;	
XX	KW	wound healing; stroke.	
OS	Homo sapiens.		
XX	US2004018196-A1.		
XX	29-JAN-2004.		
XX	11-JAN-2002; 2002US-00044564.		
XX	11-JAN-2001; 2001US-0261013P.		
XX	11-JAN-2001; 2001US-0261014P.		
XX	11-JAN-2001; 2001US-0261018P.		
XX	11-JAN-2001; 2001US-0261026P.		
XX	17-AUG-2001; 2001US-0313170P.		
XX	10-SEP-2001; 2001US-0318410P.		
XX	(MEZE/) MEZES P. D.		
PA	(RAST/) RASTELLI L.		
PA	(HERR/) HERRMANN J. L.		
PA	(MACD/) MACDOUGALL J. R.		
PA	(ZHON/) ZHONG H.		
PA	(CASM/) CASMAN S. J.		
PA	(BOLD/) BOLD F. L.		
PA	(SHIM/) SHIMKETS R. A.		
PA	(GORM/) GORMAN L.		
PA	(EISE/) EISEN A. J.		
PA	(SPAD/) SPADERNA S. K.		
PA	(VERN/) VERNET C. A. M.		
PA	(BERG/) BERGHS C.		
PA	(SPYT/) SPYTEK K. A.		
PA	(DIP1/) DIPIPPO V. A.		
PA	(ZERH/) ZERHUSEN B. D.		

PA	(PEYM/) PEYMAN J. A.		
PA	(ELLE/) ELLERMAN K.		
PA	(STON/) STONE D. J.		
PA	(GROS/) GROSSE W. M.		
PA	(ALSO/) ALSOBROOK J. P.		
PA	(LEPL/) LEPLEY D. M.		
PA	(RIEG/) RIEGER D. K.		
PA	(BURG/) BURGESS C. E.		
PA	(EDIN/) EDINGER S. R.		
XX	Mezes PD, Rastelli L, Herrmann JL, Macdougall JR, Zhong H;		
PI	Caaman SJ, Boldog FL, Shimkets RA, Eisen AJ, Spaderna SK;		
PI	Vernet CAM, Berghs C, Spytke KA, Dipippo VA, Zerhusen BD, Peyman JA;		
PI	Ellerman K, Stone DJ, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK;		
XX	Burgess CB, Edinger SR;		
DR	WPI; 2004-121988/12.		
DR	P-PSDB; ADO39192.		
XX	New isolated SECX polypeptides and polynucleotides, useful for treating or preventing, e.g. cardiomyopathy, atherosclerosis, obesity, prostate cancer, hemophilia, graft versus host disease, Crohn's disease, multiple sclerosis or psoriasis.		
XX	Disclosure; SEQ ID NO 17; 306pp; English.		
XX	The invention relates to a method of treating or delaying the onset of an angiogenic-associated disorder comprising administering an antibody to the polypeptide of SEC1. The cDNAs and proteins for SEC1-SEC12 are disclosed as new. Also included are an isolated NOVX (NOV1-NOV8) polypeptide (or its mature form or variant), the encoding nucleic acid for the NOVX protein described above, a vector comprising the nucleic acid molecule, a cell comprising the vector, an antibody that binds immunospecifically to NOVX, a method of treating or delaying the onset of an angiogenic-associated disorder, a method for determining the presence of or predisposition to a disease associated with altered levels of SEC1 (or altered levels of the nucleic acid of SEC1 in a first mammalian subject), a method for determining the presence of or predisposition to a disease associated with altered levels of SEC1-SEC12, a method of treating a pathological state in a mammal, a method of treating or delaying the onset of a disorder, a method for determining the presence or amount of the polypeptide or nucleic acid, a method of identifying an agent that binds to a polypeptide, a method for identifying an agent that modulates the expression or activity of the polypeptide, a method for modulating the activity of the polypeptide, a method of treating or preventing a SECX-associated or NOVX disorder, a pharmaceutical composition (comprising NOVX or SECX, the nucleic acid molecule or the antibody and a pharmaceutical carrier), a kit comprising (in one or more containers) the pharmaceutical composition and a method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide or the nucleic acid in a first mammalian subject. The SECX/NOVX polypeptides and polynucleotides are useful for cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect, valve disease, tuberosus sclerosis, scleroderma, obesity, transplantation, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, haemophilia, hypercoagulation, idiopathic thrombocytopaenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease or multiple sclerosis. They are also useful for treating angiogenic-associated disorders including psoriasis, wound healing or stroke. The present sequence encodes a SECX protein.		
XX	Sequence 1192 BP; 262 A; 349 C; 335 G; 245 T; 0 U; 1 Other;		

Query Match		99.9%;	Score 1191;	DB 12;	Length 1192;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1191;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	CCAGCCCGAAAGCAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTTCCTCTGCTGCC	60		
Db	1	CCAGCCCGAAAGCAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTTCCTCTGCTGCC	60		

Qy 61 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTGCTGGTTCTGATTTCTCCAGCGTGC 120
Db 61 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTGCTGGTTCTGATTTCTCCAGCGTGC 120

Qy 121 GTGGTTGTGGAATGCAACCGCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 121 GTGGTTGTGGAATGCAACCGCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTCCTTACGAGGACTCCCT 240
Db 181 ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTCCTTACGAGGACTCCCT 240

Qy 241 CACCTGGTCAATGCAGCGGACGTAACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300
Db 241 CACCTGGTCAATGCAGCGGACGTAACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300

Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGAGCACAGTGGCGGTATGAAGAG 360
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGAGCACAGTGGCGGTATGAAGAG 360

Qy 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTTCGCCACGACCATGTTGGCCAC 420
Db 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTTCGCCACGACCATGTTGGCCAC 420

Qy 421 GGACAGAGCGAAGGGAGAGATGTAAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480
Db 421 GGACAGAGCGAAGGGAGAGATGTAAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480

Qy 481 TTGAGCATGTGGATTTCCATGCAGAAAGACTACCTGGGCTTCTGTCTTCTTCTGGGC 540
Db 481 TTGAGCATGTGGATTTCCATGCAGAAAGACTACCTGGGCTTCTGTCTTCTTCTGGGC 540

Qy 541 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCGAGAGCGCGGGCCACTTCGCC 600
Db 541 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCGAGAGCGCGGGCCACTTCGCC 600

Qy 601 GGCATGTGACTCATTTGGCCCTTGGTCTTCCCAATCTGGAATCTGCAACAACTTCAAG 660
Db 601 GGCATGTGACTCATTTGGCCCTTGGTCTTCCCAATCTGGAATCTGCAACAACTTCAAG 660

Qy 661 GTCCTTGTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCGCCATCGAC 720
Db 661 GTCCTTGTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCGCCATCGAC 720

Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATACTCAGACCCCTGTATC 780
Db 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATACTCAGACCCCTGTATC 780

Qy 781 TGCCGGGCGAGGCTGCAAGGTGCTTGGGCATCCAACTGCTGAATGCGGTCTCAGCGGTG 840
Db 781 TGCCGGGCGAGGCTGCAAGGTGCTTGGGCATCCAACTGCTGAATGCGGTCTCAGCGGTG 840

Qy 841 GAGCGCGCCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900
Db 841 GAGCGCGCCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900

Qy 901 CTATGTGACAGCAAGGGCCCTA CTGTCTCATGAGTTAGCCAAAGCAGGACAAGACT 960
Db 901 CTATGTGACAGCAAGGGCCCTA CTGTCTCATGAGTTAGCCAAAGCAGGACAAGACT 960

Qy 961 CTCAGATTTATGAGGTGCTCAACATGTTCTTCCACAGGAGCTTCTGGAAGTCAACAC 1020
Db 961 CTCAGATTTATGAGGTGCTCAACATGTTCTTCCACAGGAGCTTCTGGAAGTCAACAC 1020

Qy 1021 TCCGTCTTCCATGAAATAAATGTGGTCTCTCAAAGGACAGCCACGCGAGGAAGTCCG 1080
Db 1021 TCCGTCTTCCATGAAATAAATGTGGTCTCTCAAAGGACAGCCACGCGAGGAAGTCCG 1080

Qy 1081 TCCCCACCTGAATGCAATGGCCGGTGCCTGGCTCATGGTCTGGGGATGACGAGGG 1140
Db 1081 TCCCCACCTGAATGCAATGGCCGGTGCCTGGCTCATGGTCTGGGGATGACGAGGG 1140

Qy 1141 AAGGCGAGATGGCTTCTCAGATATGGCTTGCACAAAAA 1192
Db 1141 AAGGCGAGATGGCTTCTCAGATATGGCTTGCACAAAAA 1192

RESULT 9
ADL56807
ID ADL56807 standard; cDNA; 1192 BP.
XX ADL56807;
AC
XX
DT 20-MAY-2004 (first entry)
XX
DE Human SECX cDNA #9.
XX
KW Human; SECX; gene; ss; angiogenic-associated disorder; cancer;
KW cardiovascular disease; psoriasis; wound healing; stroke; cardiomyopathy;
KW atherosclerosis; cell signal processing disorder;
KW metabolic pathway modulation disorder; diabetes;
KW hyperproliferative disease; cirrhosis; keloid; psoriasis; osteoarthritis;
KW haemorrhage; ischaemic heart disease; renal disease; thrombosis;
KW hypertension; hypothyroidism; autoimmune disorder; multiple sclerosis;
KW systemic lupus erythematosus; rheumatoid arthritis;
KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;
KW autoimmune thyroiditis; myasthenia gravis; graft-versus-host disease;
KW asthma, periodontal disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis; shy-drager syndrome.
XX
OS Homo sapiens.
XX
US2003215449-A1.
XX
PD 20-NOV-2003.
XX
PF 15-MAR-2002; 2002US-00099322.
XX
PR 11-JAN-2001; 2001US-0261013P.
PR 11-JAN-2001; 2001US-0261014P.
PR 11-JAN-2001; 2001US-0261018P.
PR 11-JAN-2001; 2001US-0261026P.
PR 11-JAN-2001; 2001US-0261029P.
PR 23-MAR-2001; 2001US-0278152P.
PR 17-AUG-2001; 2001US-0313170P.
PR 10-SEP-2001; 2001US-0318410P.
PR 11-JAN-2002; 2002US-00044564.
XX
PA (MEZE/) MEZES P D.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASW/) CASMAN S J.
PA (BOLD/) BOLDIG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGS C.
PA (SPYT/) SPYTEK K A.
PA (DIP1/) DIPIPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYW/) PEYMAN J A.
PA (ELLER/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
PA (VOSS/) VOSS E Z.
PA (MILL/) MILLER C E.

XX Mezes PD, Rastelli L, Herrmann JL, Macdougall JR, Zhong H;
PI Casman SJ, Boldog FL, Shimkets RA, Gorman L, Eisen AJ, Spaderna SK;
PI Vernet KM, Berghs C, Spytek KA, Dipippo VA, Zerhusen BD, Peyman JA;
PI Ellerman K, Stone DJ, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK;
PI Burgess CE, Edinger SR, Voss EZ, Miller CE;
XX WPI; 2004-130990/13.
DR P-ESDB; ADL56808.
XX Novel isolated SEC1 and/or NOVX polypeptide, useful for treating cancer,
PT cardiovascular disease, psoriasis, wound healing, and stroke.
XX Disclosure; SEQ ID NO 17; 315pp; English.
XX The invention relates to human SECX and NOVX polypeptides and the
CC polynucleotides encoding them. The invention also relates to antibodies
CC that bind immunospecifically to the polypeptides. The sequences are
CC useful for treating or preventing angiogenic-associated disorders,
CC cancer, cardiovascular disease, psoriasis, wound healing, stroke,
CC cardiomyopathy, atherosclerosis, cell signal processing disorders,
CC metabolic pathway modulation disorders, diabetes, hyperproliferative
CC diseases, cirrhosis, keloids, psoriasis, osteoarthritis, atherosclerotic
CC plaque formation, haemorrhage, ischaemic heart disease, renal disease,
CC thrombosis, hypertension, hypothyroidism, autoimmune disorders, multiple
CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
CC pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis,
CC myasthenia gravis, graft-versus-host disease, asthma, periodontal
CC disease, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis and shy-draeger syndrome. This sequence
CC represents a human SECX polynucleotide of the invention.

XX SQ Sequence 1192 BP; 262 A; 365 C; 319 G; 245 T; 0 U; 1 Other;

Query Match 97.9%; Score 1167; DB 12; Length 1192;

Best Local Similarity 98.7%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CCAGCCGAAAGGAGGCTCGGGTGGCGGAAGAGGGCTCGAGCTGCTTCCTCGTGGCC 60
Db 1 CCAGCCGAAAGGAGGCTCGGGTGGCGGAAGAGGGCTCGAGCTGCTTCCTCGTGGCC 60
Qy 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTGCTCGTGGTTCCTCAGGCTGTC 120
Db 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTGCTCGTGGTTCCTCAGGCTGTC 120
Qy 121 GTGGTTGTGGAATGAAACGCGCAGACATATGAAACAGAGCTGAGACCTTCCAGC 180
Db 121 GTGGTTGTGGAATGAAACGCGCAGACATATGAAACAGAGCTGAGACCTTCCAGC 180
Qy 181 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGCAGAGCATTCCTACCGAGCTCCCT 240
Db 181 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGCAGAGCATTCCTACCGAGCTCCCT 240
Qy 241 CACCTGTCTAATGACAGCGACAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
Db 241 CACCTGTCTAATGACAGCGACAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGCAGACAGTGGCCGCTATGAAGAG 360
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGCAGACAGTGGCCGCTATGAAGAG 360
Qy 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 GGACAGAGCGAAGGGAGAGGATGCTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480
Db 421 GGAAGAGCGAAGGGAGAGGATGCTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480
Qy 481 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTTCGCGC 540
Db 481 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTTCGCGC 540

Qy 541 CACTCCATGGAGCGCGCCATCGCCATCCTCAOCCGCCGACAGAGAGCGCGGCGCACTTCGCC 600
Db 541 CACTCCATGGAGCGCGCCATCGCCATCCTCAOCCGCCGACAGAGAGCGCGGCGCACTTCGCC 600
Qy 601 GGCATGCTACTCATTTTCGCTCTGGTTCCTTGGCCATCCTGAACTGCAACAACTTTCAAG 660
Db 601 GGCATGCTACTCATTTTCGCTCTGGTTCCTTGGCCATCCTGAACTGCAACAACTTTCAAG 660
Qy 661 GTCCTTCTCGAAAGTGCTCAACCTTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720
Db 661 GTCCTTCTCGAAAGTGCTCAACCTTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGCTCGACATTTATAACTCAGACCCCTCGATC 780
Db 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGCTCGACATTTATAACTCAGACCCCTCGATC 780
Qy 781 TGCCGGCAGCGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCGCTTCACGGGTG 840
Db 781 TGCCGGCAGCGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCGCTTCACGGGTG 840
Qy 841 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGCGCTCTGCCGATCGC 900
Db 841 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGCGCTCTGCCGATCGC 900
Qy 901 CTATGTGACAGCAAAAGGGGCTTACTCTGCTCATGAGTTAGCCAGAGCCAGGCAAGACT 960
Db 901 CTATGTGACAGCAAAAGGGGCTTACTCTGCTCATGAGTTAGCCAGAGCCAGGCAAGACT 960
Qy 961 CTCAGATTTATGAGGTGCTTACCATGTTCTTCCAGAGGAGTTCCTGAAGTCAACAC 1020
Db 961 CTCAGATTTATGAGGTGCTTACCATGTTCTTCCAGAGGAGTTCCTGAAGTCAACAC 1020
Qy 1021 TCCGTCTTCCATGAAATAAATGATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080
Db 1021 TCCGTCTTCCATGAAATAAATGATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080
Qy 1081 TCCCCACCTCTGAATGCAATTTGGCCGGTCCCGGCTCATGGTCTGGGGGATGCGAGCGGG 1140
Db 1081 TCCCCACCTCTGAATGCAATTTGGCCGGTCCCGGCTCATGGTCTGGGGGATGCGAGCGGG 1140
Qy 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1192
Db 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1192

RESULT 10

AAS94886

ID AAS94886 standard; DNA; 4193 BP.

XX AC AAS94886;

XX AC AAS94886;

DT 14-FEB-2002 (first entry)

XX Human DNA sequence #141 expressed during foam cell differentiation.

XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;

XX cardiovascular disorder; coronary artery disease; gene therapy; ds.

XX Homo sapiens.

XX WO200177389-A2.

XX 18-OCT-2001.

XX 04-APR-2001; 2001WO-US011128.

XX 05-APR-2000; 2000US-0195106P.

XX (INCY-) INCYTE GENOMICS INC.

XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;

PI Tai J;

XX WPI; 2002-010925/01.
DR
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development.
XX
PS Claim 1; Page 197-198; 315pp; English.
XX
CC The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used as
CC PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. A894746-A895021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation
XX
SQ Sequence 4193 BP; 904 A; 1264 C; 1116 G; 885 T; 0 U; 24 Other;
Query Match 97.5%; Score 1162; DB 6; Length 4193;
Best Local Similarity 99.9%; Pred. No. 3.7e-313;
Matches 1173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CCAGCCCCAAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCTTCCTGCTGCC 60
Db 452 CCAGCCCCAAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCTTCCTGCTGCC 511
Qy 61 TTGGGGCGCCGACGATGAGGAAACAGCCCGATTTGCTGGTTCGATTCACAGGCTGC 120
Db 512 TTGGGGCGCCGACGATGAGGAAACAGCCCGATTTGCTGGTTCGATTCACAGGCTGC 571
Qy 121 GTGGTTGGGAATGCAAAACCCAGCAGCATATGGAACAGCAGCCTGAGACCTTCACG 180
Db 572 GTGGTTGGGAATGCAAAACCCAGCAGCATATGGAACAGCAGCCTGAGACCTTCACG 631
Qy 181 ATGCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTACCGAGCTCCCT 240
Db 632 ATGCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTACCGAGCTCCCT 691
Qy 241 CACTGTGTCATGACGAGCAGTACCTCTTCTGCAAGTACT-GGAAACCCACAGGCAC 299
Db 692 CACTGTGTCATGACGAGCAGTACCTCTTCTGCAAGTACTGCGAAACCCACAGGCAC 751
Qy 300 ACCCAGGCCCTCATCTTTGTGCCATGGAGCGGAGCAGCAGTGGCGCTATGAGA 359
Db 752 ACCCAGGCCCTCATCTTTGTGCCATGGAGCGGAGCAGCAGTGGCGCTATGAGA 811
Qy 360 GCTGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCATTGTTGCCA 419
Db 812 GCTGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCATTGTTGCCA 871
Qy 420 CGGACAGACGAAAGGGAGAGATGGTGTAGTCTGTGACTTCACGTTTTCGTACGGATGT 479
Db 872 CGGACAGACGAAAGGGAGAGATGGTGTAGTCTGTGACTTCACGTTTTCGTACGGATGT 931
Qy 480 GTTCAGCATGTGGATTCATGCGAAGAGATACCTCTGGGCTTCTGTCTTCTCTGGG 539
Db 932 GTTCAGCATGTGGATTCATGCGAAGAGATACCTCTGGGCTTCTGTCTTCTCTGGG 991
Qy 540 CCACCTCCATGGAGCGGCATCGCCATCCTCAGCGCCCGCAGAGAGCGCGGCCACTTCGC 599
Db 992 CCACCTCCATGGAGCGGCATCGCCATCCTCAGCGCCCGCAGAGAGCGCGGCCACTTCGC 1051
Qy 600 CGGCATGTGATCATATTCCTGCTGTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Db 1052 CGGCATGTGATCATATTCCTGCTGTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111

Qy 660 GGTCTTGTCTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCTCCTCGGCCCATCGA 719
Db 1112 GGTCTTGTCTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCTCCTCGGCCCATCGA 1171
Qy 720 CTCACGCGTCTCTCTCGGAATAAGACAGAGGTGCGACATTATTAACCTCAAGCCCTGTAT 779
Db 1172 CTCACGCGTCTCTCTCGGAATAAGACAGAGGTGCGACATTATTAACCTCAAGCCCTGTAT 1231
Qy 780 CTGCGCGGACAGGCTGAGGTGTCTTCGGCATCCAACTGCTGAATGCCCTCTCACGGGT 839
Db 1232 CTGCGCGGACAGGCTGAGGTGTCTTCGGCATCCAACTGCTGAATGCCCTCTCACGGGT 1291
Qy 840 GGAGCGCGCCTCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCG 899
Db 1292 GGAGCGCGCCTCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCG 1351
Qy 900 CCTATGTGACAGCAAAAGGGCCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGAC 959
Db 1352 CCTATGTGACAGCAAAAGGGCCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGAC 1411
Qy 960 TCTCAAGATTATCAAGGTGCTTACCATTGTTCTCCAAAGAGCTTCTGAGTCAACCAA 1019
Db 1412 TCTCAAGATTATCAAGGTGCTTACCATTGTTCTCCAAAGAGCTTCTGAGTCAACCAA 1471
Qy 1020 CTCGCTCTTCCATAAATAACATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAATGCG 1079
Db 1472 CTCGCTCTTCCATAAATAACATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAATGCG 1531
Qy 1080 GTCCCCACCTGAATGCAATTTGGCGGTGCGCGGTCTATGTTCTGGGGATGCGAGGAGGG 1139
Db 1532 GTCCCCACCTGAATGCAATTTGGCGGTGCGCGGTCTATGTTCTGGGGATGCGAGGAGGG 1591
Qy 1140 GAAGGCGAGAGATGGCTTCTCAGATATGGCTTC 1173
Db 1592 GAAGGCGAGAGATGGCTTCTCAGATATGGCTTC 1625
RESULT 11
ADI21843
ID ADI21843 standard; cDNA; 1613 BP.
XX AC ADI21843;
XX AC
XX 15-APR-2004 (first entry)
XX DE Novel human protein cDNA #102.
XX KW forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
ss; gene.
XX Homo sapiens.
OS
XX WO2003025148-A2.
PN
XX 27-MAR-2003.
PD
XX 19-SEP-2002; 2002WO-US029964.
PP
XX 19-SEP-2001; 2001US-0323739P.
PR
XX 13-SEP-2002; 2002US-00323739.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Asundi V, Goodrich RM, Ren F, Zhang J, Zhao Q, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX WPI; 2003-354603/33.
DR P-PSDB; ADI21127.

XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.

XX Claim 1; SEQ ID NO 102; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents cDNA encoding a novel human protein.

XX SQ Sequence 1613 BP; 334 A; 465 C; 472 G; 342 T; 0 U; 0 Other;

Query Match 91.9%; Score 1096; DB 10; Length 1613;
Best Local Similarity 93.8%; Pred No. 6.1e-295;
Matches 1184; Conservative 0; Mismatches 0; Indels 78; Gaps 1;

Qy 1 CCAGCCCGAAGGCGAGGCTGGGGTGGCGGAAGAGGGCTCGAGAGTGCCTTCCTGCTGCC 60
Db 352 CCAGCCCGAAGGCGAGGCTGGGGTGGCGGAAGAGGGCTCGAGAGTGCCTTCCTGCTGCC 411
Qy 61 TTGGGGCCGCCAGATGAGGAAAGCCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC 120
Db 412 TTGGGGCCGCCAGATGAGGAAAGCCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC 471
Qy 121 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 472 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 531
Qy 181 ATGCCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTACCGAGACTCCCT 240
Db 532 ATGCCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTACCGAGACTCCCT 591
Qy 241 CACCTGTCATGACAGCGGACGATACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
Db 592 CACCTGTCATGACAGCGGACGATACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 651
Qy 301 CCCAAGGCCCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCGCGCTATGAAGAG 360
Db 652 CCCAAGGCCCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCGCGCTATGAAGAG 711
Qy 361 CTGGCTCGGATGCTGATGGGGCTGAGCTGCTGGTGTTCGCCACGACCATGTTGGCCAC 420
Db 712 CTGGCTCGGATGCTGATGGGGCTGAGCTGCTGGTGTTCGCCACGACCATGTTGGCCAC 771
Qy 421 GGACAGAGCGAAGGGAGAGATGATGCTGATCTTCCAGCTTTCGTCAGGAGATGTG 480
Db 772 GGACAGAGCGAAGGGAGAGATGATGCTGATCTTCCAGCTTTCGTCAGGAGATGTG 831
Qy 481 TTGAGGATGTGGATTCATCCAGAAAGACTACCTGGGCTTCCTGCTTCCTGCGGC 540
Db 832 TTGAGGATGTGGATTCATCCAGAAAGACTACCTGGGCTTCCTGCTTCCTGCGGC 891
Qy 541 CACTCCATGGGAGGCGCCATCGCCATCTTCAGGCGCGCAGAGAGCGCGGCGCACTTCGCC 600
Db 892 CACTCCATGGGAGGCGCCATCGCCATCTTCAGGCGCGCAGAGAGCGCGGCGCACTTCGCC 951
Qy 601 GGCAATGGTACTCATTTTCGCCCTCTGGTTCTTGGCAATCTGCAATCTGCAACCACTTCAA- 659
Db 952 GGCAATGGTACTCATTTTCGCCCTCTGGTTCTTGGCAATCTGCAATCTGCAACCACTTCAA- 1011

Qy 660 ----- 659
Db 1012 GACTATTTCGAGGATTTTGAACACTTGTGAAAAAGGCATCAAGAATGTTAAAGTTTGG 1071
Qy 660 -----GGTCTTGTGCGAAAGTGTCAACCTTGTGTCGCCAAACTTG 702
Db 1072 ATTCACAGTCCCTTTTGGGTCTTGTGCGAAAGTGTCAACCTTGTGTCGCCAAACTTG 1131
Qy 703 TCCCTCGGGGCCCATCGACTCCAGCGTCTCTCTCGGAATAGACAGAGGTGCACTTTAT 762
Db 1132 TCCCTCGGGGCCCATCGACTCCAGCGTCTCTCTCGGAATAGACAGAGGTGCACTTTAT 1191
Qy 763 AACTCAGACCCCTGATCTGCGGGCAGGGCTGAAGGTGTCTTCGGCATCCAACTGCTG 822
Db 1192 AACTCAGACCCCTGATCTGCGGGCAGGGCTGAAGGTGTCTTCGGCATCCAACTGCTG 1251
Qy 823 AATGCCCTCTCAGGGTGGAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTCCTGCTGTC 882
Db 1252 AATGCCCTCTCAGGGTGGAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTCCTGCTGTC 1311
Qy 883 CAGGGCTCTGCCGATCGCCTATGTGACAGCAAGGGGCCCTACCTGCTCATGAGTTCAGCC 942
Db 1312 CAGGGCTCTGCCGATCGCCTATGTGACAGCAAGGGGCCCTACCTGCTCATGAGTTCAGCC 1371
Qy 943 AAGAGCCAGGACAGACTCTCAAGATTTATGAAGGTGCTTACCATGTTCTCCACAAGGAG 1002
Db 1372 AAGAGCCAGGACAGACTCTCAAGATTTATGAAGGTGCTTACCATGTTCTCCACAAGGAG 1431
Qy 1003 CTTCTCAAGTCAACAACTCCGTCTTCCATGAATAAACAATGTGGGTCTCTCAAGGACA 1062
Db 1432 CTTCTCAAGTCAACAACTCCGTCTTCCATGAATAAACAATGTGGGTCTCTCAAGGACA 1491
Qy 1063 GCCACGCGAGGACTGCGTCCCACTGATGATGCGCGTGGCGGTGCGCGGTCTATGCTCT 1122
Db 1492 GCCACGCGAGGAACTGCGTCCCACTGATGATGCGCGTGGCGGTGCGCGGTCTATGCTCT 1551
Qy 1123 GGGGGATGCGAGGCGGGAAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAA 1182
Db 1552 GGGGGATGCGAGGCGGGAAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAA 1611
Qy 1183 AA 1184
Db 1612 AA 1613

RESULT 12

AAD57495
ID AAD57495 standard; cDNA; 1309 BP.

XX AAD57495;

XX 20-NOV-2003 (first entry)

XX Human enzyme (ENZM) cDNA #7.

Human; enzyme; ENZM; immune disorder; infection; myocardial infarction;
gene therapy; anaemia; acquired immune deficiency syndrome; infection;
reproductive disorder; cardiovascular; eye; cell proliferation; cancer;
AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence;
infertility; atherosclerosis; metabolic disorder; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
CDS 356..1207
/*tag= a
/product= "Human enzyme (ENZM) "

XX WO2003052075-A2.

XX 26-JUN-2003.

XX PD

XX

PF 12-DEC-2002; 2002WO-US040161.
XX
PR 14-DEC-2001; 2001US-0340357P.
PR 20-DEC-2001; 2001US-0342962P.
PR 21-DEC-2001; 2001US-0343589P.
PR 22-JAN-2002; 2002US-0351107P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R;
PI Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;
PI Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis JP;
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;
XX
XX WPI; 2003-533016/50.
DR P-PSDB; AAE38215.
DR
XX
XX New human enzyme (ENZM) polypeptide, useful for preparing a composition
PT for treating a disease associated with decreased expression or
PT overexpression of ENZM e.g. cancer.
XX
XX Claim 5; Page 315; 264pp; English.
XX
XX The invention relates to human enzyme (ENZM) polypeptides and their
CC corresponding polynucleotides. ENZM sequences are useful for preparing a
CC composition for diagnosing or treating a disease or condition associated
CC with decreased expression or overexpression of functional ENZM. The
CC disorders include immune disorders (anaemia, allergy or asthma),
CC infectious disorders (viral, fungal, parasitic or protozoal infection),
CC immune deficiencies (acquired immune deficiency syndrome; AIDS),
CC metabolic disorders (Addison's disease, diabetes or goitre), reproductive
CC disorders (infertility or impotence), cardiovascular disorders
CC (atherosclerosis or myocardial infarction), eye disorders and cell
CC proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
CC present sequence is human ENZM cDNA
XX
XX Sequence 1309 BP; 280 A; 383 C; 385 G; 261 T; 0 U; 0 Other;
XX
XX Query Match 84.1%; Score 1002; DB 9; Length 1309;
XX Best Local Similarity 92.4%; Pred. NO. 9.3e-269;
XX Matches 1102; Conservative 0; Mismatches 0; Indels 90; Gaps 1;
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QY 1 CCAGCCGAAGGAGGAGGCTCGGTGCGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC 60
DB 206 CCAGCCGAAGGAGGAGGCTCGGTGCGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC 265
QY 61 TTGGGGCCCGCCAGATGAGGAAACAGCCCGGATTTGCCCTGGTTCCTGATTTCTCCAGGCTGC 120
DB 266 TTGGGGCCCGCCAGATGAGGAAACAGCCCGGATTTGCCCTGGTTCCTGATTTCTCCAGGCTGC 325
QY 121 GTGGTTGTGGAATGCAACCGCAGACACATATGGAACACAGACCTGAAGACCTTCCAGC 180
DB 326 GTGGTTGTGGAATGCAACCGCAGACACATATGGAACACAGACCTGAAGACCTTCCAGC 385
QY 181 ATGCCAGAGGAAGTTCCTCCCGAGGAGCCCGCAGAGCATTCCTTACCAGACCTCCCT 240
DB 386 ATGCCAGAGGAAGTTCCTCCCGAGGAGCCCGCAGAGCATTCCTTACCAGACCTCCCT 445
QY 241 CACCTGGTCAATGCAGACGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGACACA 300
DB 446 CACCTGGTCAATGCAGACGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGACACA 505
QY 301 CCCAAGGCCCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCCGCTATGAAGAG 360
DB 506 CCCAAGGCCCTCATCTTTGTGTCATGAGCCGAGAGCAGTGGCCGCTATGAAGAG 565
QY 361 CTGGCTCGGATGCTGATGGGGCTGAGCCTGCTGGTGTTCGCCACAGCATGTTGGCCAC 420
DB 566 CTGGCTCGGATGCTGATGGGGCTGAGCCTGCTGGTGTTCGCCACAGCATGTTGGCCAC 625
QY 421 GGACAGACGAGGAGGAGGATGATGCTGCTGACTTCCACGTTTTCGTCAGGAGATGTG 480
DB 626 GGACAGACGAGGAGGAGGATGATGCTGCTGACTTCCACGTTTTCGTCAGGAGATGTG 685

QY 481 TTGCAGCATGTGGATTCCATGCGAAGAAGTACCTGGGGCTTCTGTCTTCTTCTTGGGC 540
DB 686 TTGCAGCATGTGGATTCCATGCGAAGAAGTACCTGGGGCTTCTGTCTTCTTCTTGGGC 745
QY 541 CACTTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGAGGCGCGGCCACTTCGCC 600
DB 746 CACTTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGAGGCGCGGCCACTTCGCC 805
QY 601 GGCATGCTACTCAATTCCTGCTTCTGGTTCCTGCAATCTGCAATCTGCAACAACTTTCAAG 660
DB 806 GGCATGCTACTCAATTCCTGCTTCTGGTTCCTGCAATCTGCAATCTGCAACAACTTTCA-- 863
QY 661 GTCCCTTCTCGGAAAGTGCTCAACCTTGTCTGTCGCAAACTTGTCCCTCGGGGCCATCGAC 720
DB 864 ----- 863
QY 721 TCCAGCGTGTCTCTCTCGGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGTGATC 780
DB 864 -----AGTTCGACATTTTATACTCAGACCCCTGTGATC 895
QY 781 TGCCGGCGAGGGCTGAAAGTGTGCTTCGGCATCCAACTGCTGTAATGCCGTCTCAACGGGTG 840
DB 896 TGCCGGCGAGGGCTGAAAGTGTGCTTCGGCATCCAACTGCTGTAATGCCGTCTCAACGGGTG 955
QY 841 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGTCTCAGGGCTCTGCCGATCGC 900
DB 956 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGTCTCAGGGCTCTGCCGATCGC 1015
QY 901 CTATGTACAGCAAGAGGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAAGCT 960
DB 1016 CTATGTACAGCAAGAGGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAAGCT 1075
QY 961 CTCGAAGATTATGAAGTGCCTACCATGTTCTCCAAAGAGGCTTCCTGAAGTCCCAAC 1020
DB 1076 CTCGAAGATTATGAAGTGCCTACCATGTTCTCCAAAGAGGCTTCCTGAAGTCCCAAC 1135
QY 1021 TCCGTCTTCCATGAATAAATGATGGTCTCTCAAAGGACAGCCAGGAGGAGCTGCG 1080
DB 1136 TCCGTCTTCCATGAATAAATGATGGTCTCTCAAAGGACAGCCAGGAGGAGCTGCG 1195
QY 1081 TCCCAACCTGAAATGCAATGGCCGCTCCCGGCTCATGCTCTGGGGGATGCAGGCAGGGG 1140
DB 1196 TCCCAACCTGAAATGCAATGGCCGCTCCCGGCTCATGCTCTGGGGGATGCAGGCAGGGG 1255
QY 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1192
DB 1256 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1307
RESULT 13
ADI21842
ID ADI21842 standard; cDNA; 1403 BP.
XX
AC ADI21842;
XX
DT 15-APR-2004 (first entry)
XX
DE Novel human protein cDNA #101.
XX
XX forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
KW ss; gene.
XX
OS Homo sapiens.
XX
FN WO2003025148-A2.
XX
PD 27-MAR-2003.
XX

PF 19-SEP-2002; 2002WO-US029964.
XX 19-SEP-2001; 2001US-0323739P.
PR 13-SEP-2002; 2002US-00323739.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX WPT; 2003-354603/33.
DR P-PSDB; ADI21126.
XX
PT New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.
XX
PS Claim 1; SEQ ID NO 101; 156pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents cDNA encoding a novel human protein.
XX
SQ Sequence 1403 BP; 276 A; 419 C; 421 G; 287 T; 0 U; 0 Other;

Query Match 79.9%; Score 952; DB 10; Length 1403;
Best Local Similarity 92.1%; Pred. No. 8.5e-255;
Matches 1052; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 1 CCAGCCGAAAGGAGGAGGCTGGGGTGGCGGAAGAGGGCTCGAGCTGCTTCCTGCTGCC 60
Db 352 CCAGCCGAAAGGAGGAGGCTGGGGTGGCGGAAGAGGGCTCGAGCTGCTTCCTGCTGCC 411

Qy 61 TTGGGGCGCCGACAGATGAGGGAACAGCCCGATTTCCTGGTTCCTGATTCCTCAGGCTGTC 120
Db 412 TTGGGGCGCCGACAGATGAGGGAACAGCCCGATTTCCTGGTTCCTGATTCCTCAGGCTGTC 471

Qy 121 GTGGTTGTGGAATGCAACGCCAGGACACATATGGAACAGAGACCTGAAGACCTCCAGC 180
Db 472 GTGGTTGTGGAATGCAACGCCAGGACACATATGGAACAGAGACCTGAAGACCTTCAGC 531

Qy 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGAGAGCATTCCTACAGGACCTCCCT 240
Db 532 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGAGAGCATTCCTACAGGACCTCCCT 591

Qy 241 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
Db 592 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 651

Qy 301 CCCAAGGCCCTCATCTTTGTGTCCATGAGCGGAGAGCAGTGGCGGCTATGAAGAG 360
Db 652 CCCAAGGCCCTCATCTTTGTGTCCATGAGCGGAGAGCAGTGGCGGCTATGAAGAG 711

Qy 361 CTGGCTCGGATGCTCATCGGGCTGACCTGCTGGTGGTTCGCCACAGACATGTTGGCCAC 420
Db 712 CTGGCTCGGATGCTCATCGGGCTGACCTGCTGGTGGTTCGCCACAGACATGTTGGCCAC 771

Qy 421 GGACAGACGGAAGGGAGAGGATGGTAGTGTCTGACTTCCAGCTTTTCGTGAGGAGATGTG 480
Db 480 GGACAGACGGAAGGGAGAGGATGGTAGTGTCTGACTTCCAGCTTTTCGTGAGGAGATGTG 480

Db 772 GGAACAGAGCGAAGGGGAGAGGATGGTAGTGTCTGACTTCCAGCTTTTCGTGAGGAGATGTG 831
Qy 481 TTGACGATGTGGATTCCATGCGAGAAAGACTTACCTGGGTTTCCTGCTTCCTTCCTGGGC 540
Db 832 TTGACGATGTGGATTCCATGCGAGAAAGACTTACCTGGGTTTCCTGCTTCCTTCCTGGGC 891
Qy 541 CACTCCATGGAGGGCGCATCGGCATCTCAGGCGCGAGAGAGCGGGCGCCTTCGCGC 600
Db 892 CACTCCATGGAGGGCGCATCGGCATCTCAGGCGCGAGAGAGCGGGCGCCTTCGCGC 951
Qy 601 GGCATGGTACTCATTTTCGCTCTGGTTCCTGCGCAATCTCTGAATCTGCAACAACCTTCAAG 660
Db 952 GGCATGGTACTCATTTTCGCTCTGGTTCCTGCGCAATCTCTGAATCTGCAACAACCTTCA-- 1009
Qy 661 GTCCTGCTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCCCTCGGGGCCCATCGAC 720
Db 1010 ----- 1009
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGATC 780
Db 1010 -----AGGTCGACATTTTATACTCAGACCCCTGATC 1041
Qy 781 TCGCGGCGAGGCTGAGGGTGTCTTCGGCATCCAACTGCTGAATGCCGTCTCACGGGTG 840
Db 1042 TCGCGGCGAGGCTGAGGGTGTCTTCGGCATCCAACTGCTGAATGCCGTCTCACGGGTG 1101
Qy 841 GAGCGGCGCTCCCAAGCTGACTGTGCTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900
Db 1102 GAGCGGCGCTCCCAAGCTGACTGTGCTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 1161
Qy 901 CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGTTAGCCAAAGAGCCAGGACAAGACT 960
Db 1162 CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGTTAGCCAAAGAGCCAGGACAAGACT 1221
Qy 961 CTCAGAGTTTATGAGGTGCTTACCATGTTCTCCACAGGAGTTCCTGAGTCAACCAAC 1020
Db 1222 CTCAGAGTTTATGAGGTGCTTACCATGTTCTCCACAGGAGTTCCTGAGTCAACCAAC 1281
Qy 1021 TCCGCTTTCATGAAATAAATCATGTGGGTCTCTCAAAGGACAGCCAGGAGGAACTCGC 1080
Db 1282 TCCGCTTTCATGAAATAAATCATGTGGGTCTCTCAAAGGACAGCCAGGAGGAACTCGC 1341
Qy 1081 TCCCAACCTTGAATGCAATTCGCGGTGCCGGCTCATGGTCTGGGGATGACGAGGAGG 1140
Db 1342 TCCCAACCTTGAATGCAATTCGCGGTGCCGGCTCATGGTCTGGGGATGACGAGGAGG 1401
Qy 1141 AA 1142
Db 1402 AA 1403

RESULT 14
ABV99414
ID ABV99414 standard; DNA; 895 BP.
XX AC ABV99414;
XX AC ABV99414;
DT 27-JAN-2003 (first entry)
XX Human NOV42a coding sequence.
XX Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS;
XX anti-inflammatory; cardiac; haemostatic; neuroprotective; anorectic;
XX norepinephrine; immunosuppressive; osteopathic; antiparkinsonian; cancer;
XX antifertility; cerebroprotective; gene therapy; NOX; NOV; fertility;
XX metabolic disorder; diabetes; obesity; infectious disease; anorexia;
XX neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
XX immune disorder; haematopoietic disorder; cardiovascular disorder;
XX bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis;
XX metabolic syndrome X; wasting disorder; cell differentiation;
XX single nucleotide polymorphism; SNP; cell proliferation; haematopoiesis;
XX wound healing; angiogenesis; gene; ds.

OS	Homo sapiens.	
XX	Key	Location/Qualifiers
PH	variation	replace(698,G)
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
XX		
PN	W0200272771-A2.	
XX		
XX	19-SEP-2002.	
PD		
XX	08-MAR-2002; 2002WO-US007288.	
XX		
PR	08-MAR-2001; 2001US-0274101P.	
PR	08-MAR-2001; 2001US-02741194P.	
PR	08-MAR-2001; 2001US-0274281P.	
PR	08-MAR-2001; 2001US-0274322P.	
PR	09-MAR-2001; 2001US-0274849P.	
PR	12-MAR-2001; 2001US-0275235P.	
PR	13-MAR-2001; 2001US-0275578P.	
PR	13-MAR-2001; 2001US-0275579P.	
PR	13-MAR-2001; 2001US-0275601P.	
PR	14-MAR-2001; 2001US-0276000P.	
PR	16-MAR-2001; 2001US-0276776P.	
PR	19-MAR-2001; 2001US-0276994P.	
PR	20-MAR-2001; 2001US-0277239P.	
PR	20-MAR-2001; 2001US-0277321P.	
PR	20-MAR-2001; 2001US-0277327P.	
PR	20-MAR-2001; 2001US-0277338P.	
PR	21-MAR-2001; 2001US-0277791P.	
PR	22-MAR-2001; 2001US-0277833P.	
PR	23-MAR-2001; 2001US-0278152P.	
PR	26-MAR-2001; 2001US-0278894P.	
PR	27-MAR-2001; 2001US-0278999P.	
PR	27-MAR-2001; 2001US-0279036P.	
PR	28-MAR-2001; 2001US-0279344P.	
PR	30-MAR-2001; 2001US-0279995P.	
PR	30-MAR-2001; 2001US-0280233P.	
PR	02-APR-2001; 2001US-0280802P.	
PR	02-APR-2001; 2001US-0280802P.	
PR	04-APR-2001; 2001US-0280900P.	
PR	04-APR-2001; 2001US-0281194P.	
PR	13-APR-2001; 2001US-0283675P.	
PR	30-APR-2001; 2001US-0287424P.	
PR	02-MAY-2001; 2001US-0288066P.	
PR	03-MAY-2001; 2001US-0288066P.	
PR	03-MAY-2001; 2001US-0288528P.	
PR	15-MAY-2001; 2001US-0291190P.	
PR	16-MAY-2001; 2001US-0291099P.	
PR	16-MAY-2001; 2001US-0291240P.	
PR	30-MAY-2001; 2001US-0294485P.	
PR	31-MAY-2001; 2001US-0294889P.	
PR	31-MAY-2001; 2001US-0294899P.	
PR	18-JUN-2001; 2001US-0299027P.	
PR	19-JUN-2001; 2001US-0299303P.	
PR	19-JUN-2001; 2001US-0299310P.	
PR	10-JUL-2001; 2001US-0304354P.	
PR	31-JUL-2001; 2001US-0309198P.	
PR	16-AUG-2001; 2001US-0312903P.	
PR	10-SEP-2001; 2001US-0318462P.	
PR	12-SEP-2001; 2001US-0318770P.	
PR	27-SEP-2001; 2001US-0325430P.	
PR	27-SEP-2001; 2001US-0325681P.	
PR	18-OCT-2001; 2001US-0330380P.	
PR	31-OCT-2001; 2001US-0335301P.	
PR	14-NOV-2001; 2001US-0332172P.	
PR	14-NOV-2001; 2001US-0332271P.	
PR	14-NOV-2001; 2001US-0332272P.	
PR	14-NOV-2001; 2001US-0333184P.	
PR	14-NOV-2001; 2001US-0333272P.	
PR	21-NOV-2001; 2001US-0332094P.	
PR	03-DEC-2001; 2001US-0337426P.	
PR	03-DEC-2001; 2001US-0338092P.	

PR	04-DEC-2001; 2001US-0337185P.	
PR	03-JAN-2002; 2002US-0345705P.	
PR	08-MAR-2002; 2002US-00093463.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Rastelli L, Mezes PD, Smitheon G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigar M, Shenoy SG, Kekuda R, Gusev VV, Pochart PF; Zhong M;	
XX		
DR	WPI; 2002-732824/79.	
DR	P-PSDB; ABP70136.	
XX		
PT	New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.	
PT		
PT		
XX		
PS	Claim 16; Page 253; 619pp; English.	
XX		
CC	The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV95327-ABV9595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods	
XX		
SQ	Sequence 895 BP; 195 A; 274 C; 240 G; 186 T; 0 U; 0 Other;	
	Query Match 66.4%; Score 791.8; DB 6; Length 895;	
	Best Local Similarity 90.7%; Pred. No. 3.5e-210;	
	Matches 893; Conservative 0; Mismatches 2; Indels 90; Gaps 1;	
Qy	116 CTGTCGTGGTGTGGATGCAAAAGCCAGCACATATGGAACAGGACCTGAGACCCCTT 175	
Db	1 CTGTCGTGGTGTGGATGCAAAAGCCAGCACATATGGAACAGGACCTGAGACCCCTT 60	
Qy	176 CCAGCATGCCAGAGGAAAGTTCCCCAGGGGACCCCGCAGAGCATTTCCCTACCAGGACC 235	
Db	61 CCAGCATGCCAGAGGAAAGTTCCCCAGGGGACCCCGCAGAGCATTTCCCTACCAGGACC 120	
Qy	236 TCCCTACCTGGTCAATGCGAGCGACAGTACCTCTTCTGCGAGGTACTGGAACCCACAG 295	
Db	121 TCCCTACCTGGTCAATGCGAGCGACAGTACCTCTTCTGCGAGGTACTGGAACCCACAG 180	
Qy	296 GCACACCAAGGCCCTCATCTTTGTGTCCCATGAGCGCGAGAGCACAGTGGCCGCTATG 355	
Db	181 GCACACCAAGGCCCTCATCTTTGTGTCCCATGAGCGCGAGAGCACAGTGGCCGCTATG 240	
Qy	356 AAGAGCTGGCTCGGATGCTGATGGGCTGGACCTGTGGTGTTCGCCACGACCATGTTG 415	
Db	241 AAGAGCTGGCTCGGATGCTGATGGGCTGGACCTGTGGTGTTCGCCACGACCATGTTG 300	
Qy	416 GCCACGACAGAGCGAAGGGGAGAGGATGCTAGTCTGCTTCCAGCTTTTCTGTCAGGG 475	
Db	301 GCCACGACAGAGCGAAGGGGAGAGGATGCTAGTCTGCTTCCAGCTTTTCTGTCAGGG 360	

Qy	476	ATGTGTTGCAGCATGTGATTCCATGCGAAGAAGACTACCTGGGCTTCCTGTCCTCCCTC	535
Db	361	ATGTGTTGCAGCATGTGATTCCATGCGAAGAAGACTACCTGGGCTTCCTGTCCTCCCTC	420
Qy	536	TGGGCCACTCCATGGGAGCGCCATCGGCATCCTCAACGGCCGACAGAGAGCGCGGCCACT	595
Db	421	TGGGCCACTCCATGGGAGCGCCATCGGCATCCTCAACGGCCGACAGAGAGCGCGGCCACT	480
Qy	596	TCGCGGGCATGGTACTCATTTGCGCTCTGGTTCTTGGCAATCCTGAATCTGCAACAACCT	655
Db	481	TCGCGGGCATGGTACTCATTTGCGCTCTGGTTCTTGGCAATCCTGAATCTGCAACAACCT	540
Qy	656	TCAAGGTCCTTGCTGCGAAGTGCTCAACCTGTGCTGCCAAACTGTGCCCTCGGGGCCA	715
Db	541	TCA-----	543
Qy	716	TCGACTCCAGCGTGCTCTTCGGAAATAGACAGAGGTGCAATTTATAACTCAGACCCCC	775
Db	544	-----AGTTCGACATTTATAACTCAGACCCCC	570
Qy	776	TGATCTGCGGGCAGGGCTGAAGGTGTGCTTCGGCATCCAACTGTCTGAATGCGGTCTCAC	835
Db	571	TGATCTGCGGGCAGGGCTGAAGGTGTGCTTCGGCATCCAACTGTCTGAATGCGGTCTCAC	630
Qy	836	GGGTGGAGCGCGCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTCCAGGGCTCTGCGG	895
Db	631	GGGTGGAGCGCGCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTCCAGGGCTCTGCGG	690
Qy	896	ATCGCTTATGTGACAGCAAAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACA	955
Db	691	ATCGCTTATGTGACAGCAAAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGACCCAGGACA	750
Qy	956	AGACTCTCAAGATTATGAAGGTGCTTACCATTGTTCTCCAAAGAGAGCTTCTGTAAGTCA	1015
Db	751	AGACTCTCAAGATTATGAAGGTGCTTACCATTGTTCTCCAAAGAGAGCTTCTGTAAGTCA	810
Qy	1016	CCAACTCGCTCTTCCATGAAATAAACATGTGGGTCTCTCAAAGGACAGCAGCGGAGGAA	1075
Db	811	CCAACTCGCTCTTCCATGAAATAAACATGTGGGTCTCTCAAAGGACAGCAGCGGAGGAA	870
Qy	1076	CTGCGTCCCCACCTGGAATGATTG	1100
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[illegible]

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OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363.4	30.5	517	US-09-621-976-3521	Sequence 3521, Ap
2	183.4	15.4	489	US-09-621-976-126	Sequence 126, App
3	116.2	9.7	4403765	US-09-103-840A-2	Sequence 2, Appli
4	116.2	9.7	4411529	US-09-103-840A-1	Sequence 1, Appli
5	51.2	4.3	402	US-09-060-756-652	Sequence 652, App
6	51.2	4.3	402	US-09-670-314-652	Sequence 652, App
7	48.4	4.1	15572	US-09-902-540-1131	Sequence 1131, Ap
8	43.4	3.6	534	US-09-252-991A-5873	Sequence 5873, Ap
9	43.4	3.6	1968	US-09-252-991A-5829	Sequence 5829, Ap
10	43.4	3.6	2190	US-09-253-991A-5779	Sequence 5779, Ap
11	39	3.3	832	US-09-621-976-2813	Sequence 2813, Ap
12	39	3.3	865	US-09-280-116-63	Sequence 63, Appl
13	39	3.3	1125	US-09-252-991A-11202	Sequence 11202, A
14	38.8	3.3	505	US-09-621-976-15639	Sequence 15639, A
15	38.6	3.2	705	US-09-796-110-3	Sequence 3, Appli
16	38.6	3.2	2830	US-09-010-928B-1	Sequence 1, Appli
17	38.6	3.2	7218	US-08-232-463-14	Sequence 14, Appl
18	38.2	3.2	276	US-09-313-294A-3547	Sequence 3547, Ap
19	38	3.2	1768	US-09-485-529-13	Sequence 13, Appl
20	38	3.2	2125	US-09-485-529-14	Sequence 14, Appl
21	37.8	3.2	789	US-08-602-359A-28	Sequence 28, Appl
22	37.6	3.2	865	US-09-796-110-1	Sequence 1, Appli
23	37.6	3.2	866	US-09-620-312D-482	Sequence 482, App
24	37.4	3.1	6047	US-09-902-540-758	Sequence 758, App
25	37	3.1	8438	US-07-945-283-1	Sequence 1, Appli
26	36.6	3.1	9208	US-09-068-506-1	Sequence 1, Appli
27	36.4	3.1	840	US-09-902-540-3440	Sequence 3440, Ap

28	36.4	3.1	1812	4	US-09-252-991A-1140	Sequence 1140, Ap
29	36.4	3.1	1890	4	US-09-252-991A-942	Sequence 942, App
30	36.4	3.1	2001	4	US-09-252-991A-891	Sequence 891, Appl
31	36.4	3.1	2255	4	US-09-485-529-15	Sequence 15, Appl
32	36.4	3.1	19726	4	US-09-902-540-1164	Sequence 1164, Ap
33	36	3.0	954	4	US-09-252-991A-13383	Sequence 13383, A
34	36	3.0	1057	4	US-09-949-016-4554	Sequence 4554, Ap
35	36	3.0	1430	3	US-09-492-985-1	Sequence 1, Appli
36	36	3.0	1536	4	US-09-252-991A-11693	Sequence 11693, A
37	36	3.0	2103	4	US-09-252-991A-11773	Sequence 11773, A
38	36	3.0	49301	4	US-09-949-016-16296	Sequence 16296, A
39	35.8	3.0	1471	3	US-09-492-985-11	Sequence 11, Appl
40	35.8	3.0	18152	4	US-09-949-016-16849	Sequence 16849, A
41	35.6	3.0	1128	4	US-09-622-439-1	Sequence 1, Appli
42	35.6	3.0	1128	4	US-10-318-142-1	Sequence 1, Appli
43	35.6	3.0	72455	4	US-09-949-016-13793	Sequence 13793, A
44	35.6	3.0	104475	4	US-09-949-016-12115	Sequence 12115, A
45	35.6	3.0	111282	3	US-09-754-250-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-3521
; Sequence 3521, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3521
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..494
US-09-621-976-3521

Query Match	30.5%	Score	363.4	DB	4	Length	517
Best Local Similarity	98.7%	Pred. No.	4.7e-94				
Matches	372	Conservative	4	Mismatches	0	Indels	1
Gaps	1						
Qy	1	CCAGCCCGAAGGAGGAGGTC	TGGGTGGGGAAGAGGGCTCGAGCTGCTTCTCTGCTGCC	60			
Db	141	CCAGCCCGAAGGAGGAGGTC	TGGGTGGGGAAGAGGGCTCGAGCTGCTTCTCTGCTGCC	200			
Qy	61	TTGGGGCGCCCGACATGAGG	AAACAGCCCGATTTGCTTGTCTGATTTCTCAGGCTGTC	120			
Db	201	TTGGGGCGCCCGACATGAGG	AAACAGCCCGATTTGCTTGTCTGATTTCTCAGGCTGTC	260			
Qy	121	GTGTTGTGGTAATGAAACGC	CACACATATGAAACAGGACCTTGAAGACCTTCCAGC	180			
Db	261	GTGTTGTGGTAATGAAACGC	CACACATATGAAACAGGACCTTGAAGACCTTCCAGC	320			
Qy	181	ATGCCAGAGGAAAGTTCC	CCAGGAGACCCGAGAGCATTTCCCTACGAGACCTCCCT	240			
Db	321	ATGCCAGAGGAAAGTTCC	CCAGGAGACCCGAGAGCATTTCCCTACGAGACCTCCCT	380			
Qy	241	C-ACCTGGTCAATGACAG	CGGACAGTACCTTCTTCGAGGTACTTGGAAACCCACAGGAC	299			
Db	381	CAACCTGGTCAATGACAG	CGGACAGTACCTTCTTCGAGGTACTTGGAAACCCACAGGAC	440			
Qy	300	ACCAAGGCCCTCATCTT	TTGTGTCATGAGCCGAGAGCACAGTGGCCGCTATGAAGA	359			
Db	441	ACCAAGGCCCTCATCTT	TTGTGTCATGAGCCGAGAGCACAGTGGCCGCTATGAAGA	500			

```
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          9.7%; Score 116.2; DB 3; Length 4403765;
Best Local Similarity 48.3%; Pred. No. 3.7e-21;
Matches 356; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

QY 267 CCTCTCTGCGAGTACCTGGAACCCACAGGACACACCCAGGCCCTCATCTTTGTGTCCCA 326
Db 214245 CATCGTCTACAGCTCTGGACGCCGCGGACACCGGCCCAAGCGGTGTGTGTGTGGCCCA 214304

QY 327 TGGAGCCGAGAGACACAGTGGCCCGCTATGAAGAGCTGGCTCGGATGTGTATGGGCGCTGGA 386
Db 214305 TGGTCTGGCGGAGCATGCCCGCGCTACGACCATGTTCGCGAGCGGTTCGCGCGCGCGG 214364

QY 387 CTTGCTGGTGTTCGCCCAACGACCATGTTGGCCAGGACAGAGCGAAGAGGAGAGATGGT 446
Db 214365 CTTGGTCACTATGCGCTTGACCAACCGCGGCGATGGCGCTCGGGTGGCAACCGGGTGT 214424

QY 447 AGTGTCTGACTTCCACGTTTTTGTTCAGGGATGTTCGACAGATGTGGATTCATGCAGAA 506
Db 214425 AGTGAGAGACATCTCCGAGTACACCGCTGACTTTCGACACCCCTCGTTGGGATTCGCCACCCG 214484

QY 507 AGACTACCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 566
Db 214485 GGAATATCCCGGGTGCAAGCGCATCTGCTCGGGCAGACAGATGGCGCGCGCATTTGTGT 214544

QY 567 CTTACCGCGCGAGAGAGCGCGGCGCACTTCGCGGCGATGGTACTATCTATTCCTCTCTGT 626
Db 214545 CGCTTACGCTGTTCGAACGTCAGACAACTACGACCTGATGGTGC---TTTCGGCGCGCGC 214601

QY 627 TCTTGCCAACTCTGAATCTCAACAACTTTCAAGGTCTTTGCTGCGAAAGTGTCTCAACT 686
Db 214602 GGTGGCGGCGACAGACCTGTGTGAGCCCGGTAGTGGCGGTTCGCCCGCAAGCTTCTGGGCGT 214661

QY 687 TGTGCTCTCCAAACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 746
Db 214662 CGTGGTCTCCCGGCTGCGCGGTGCGAGAACTGGATTTTACTGCCATCTCTCGCGACCTGA 214721

QY 747 AGAGTGTGCAATTTATTAACCTCAGACCCCTGTATCTCGCGGCGAGGGCTGAAGTGTGCT 806
Db 214722 GGTGCTCCAGGCTTTACAAACCGACCCCACTCTGTGCACACGAGCGGTTCGCGCGCGGAT 214781

QY 807 CGGCATCCAACTGTGAATGCCGTCTCAGGGTGGAGCGGCCCTCTCCCAAGCTGACTGT 866
Db 214782 TGGCCGCGCGCTGTCTGCAAGTGGGCGAGACCATGCCCGCGGAGCACCGGCATTTACCGC 214841

QY 867 GCCCTTCTCTGTCTCCAGGGCTCTGCGGATCGCTATGTGACAGCAAGAGGGGCTACCT 926
Db 214842 GCCCTCTCTGTCTGCAAGCGGACCGATGACCGGCTGATCCCCATCAGGGGCGCGGCTG 214901

QY 927 GCTCAGGAGTTAGCCAAAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGTGCTTACCA 986
Db 214902 CTTGGTCAATGTGTGGGATCGCGCGGAGTGTGAGAGTATCCCGGGCTGTACCA 214961

QY 987 TGTCTCTCCAGGAGC 1003
Db 214962 CGAGGTGTTCAAGAGC 214978

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.

Query Match          15.4%; Score 183.4; DB 4; Length 489;
Best Local Similarity 88.6%; Pred. No. 1.9e-42;
Matches 210; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 369 GATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACGACCATGTTGGCCACGACAGAG 428
Db 254 GAAGCGGGGAGCGAGCAGCTGCTGGAACCCACCTTTTTCGACGTTGGCCACGACAGAG 313

QY 429 CGAAGGGAGAGAGTGGTGGTGTCTGACTTCCAGTTTTCGTGAGGAGTGTGTCAGCA 488
Db 314 CGAAGGGAGAGAGTGGTGGTGTCTGACTTCCACTTTTTCGTGAGGAGTGTGTCAGCA 373

QY 489 TGTGATTCATGACAGAAAGTACCTCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 548
Db 374 TGTGATTCATGACAGAAAGTACCTCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 433

QY 549 GGGAGGGCCCATCGCATCTCAGCGCGGAGAGGCGGGGCGACCTTTCGCGCGGAT 605
Db 434 GGGAGGGCCCATCG-CATCTCAGCGCGGAGAGGCGGGGCGACCTTTCGCGCGGAT 489

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
```

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103.840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 9.7%; Score 116.2; DB 3; Length 4411529;
Best Local Similarity 48.3%; Pred. No. 3.7e-21; Indels 3; Gaps 1;
Matches 356; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

Qy 267 CCTCTTCTGCAGGTACTGGAAACCCACAGGCACACCCAAAGCCCTCATCTTTGTGCCCA 326
Db 214136 CATGCTCTACGACGCTGGAGCGCGGACACCGCGCGCTGGTGTGCTGGCCCA 214195

Qy 327 TGGAGCGGAGAGACAGTGGCCGCTATGAAGAGCTGGCTCGATGCTGATGGGCTGGA 386
Db 214196 TGGTCTGGCGGAGCATGCCCGCGCTACGACCATGTGCGCAGCGGCTCGCGCGCGCGG 214255

Qy 387 CTTCTGGTGTTCGCCACGACCATGTTGGCCAGGACAGAGCAAGGGAGAGATGGT 446
Db 214256 CTTGGTCACTATGCGCTTGACCAACCGCGGCGATGGCGCTCGGGTGGCAACGGGTGCT 214315

Qy 447 AGTGTCTGACTTCCACGCTTTTCGTGAGGATGTGTGAGCATGTGATTCATCGAGAA 506
Db 214316 AGTGAGAGACATCTCGAGTACACCGCTGACTTCGACACCTCTGTGGATCGCCACCG 214375

Qy 507 AGATACCTGGGTCTCTGCTTCCTTCTGGGCACTTCATGGAGCGCGCATCGCAT 566
Db 214376 GGAATATCCCGGTCGACAGCGCATCGTCTCGGCGACAGCATGGCGCGCGCATTTGTGT 214435

Qy 567 CTTACGCGCCAGAGAGCGCGGCGCACTTCGCGGATGTGATCTCATTTCCCTCTGGT 626
Db 214436 CGCTTACGGTGTCAACGCTGACAGAACTAGACCTGATGTGC---TTTCGGCGCGCGC 214492

Qy 627 TCTTGCCAACTCCTGAATCTGCAACAACTTTCAAGTCTCTGTCGAAAGTGTCTCAACCT 686
Db 214493 GGTGGCGGACAGACCTGTGTAGCCCGGTAGTGGCGTTCCCGCAAGCTTCTGGGCGT 214552

Qy 687 TGTGCTGCAAACTGTCTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGAC 746
Db 214553 CGTGTGCGCGGCTCGCGGTGCGAGAACTGATTTTACTGCCATCTCTCGGACCCCTGA 214612

Qy 747 AGAGTTCGACATTTATTAATCAAGCCCTGATCTGCGGCGAGGCTGAAGTGTGCTT 806
Db 214613 GGTGTCCAGGCTTACAAACCGACCCCACTCGTGACACAGGAGGGTTCCGCGCGGGAT 214672

Qy 807 CGGATCCAACTGTGTAATCGGCTCTACAGGTGGAGCGCGCCCTCCCAAGCTGACTGT 866
Db 214673 TGGCGCGCGTGTGTGAGGTGGGGGAGACCATGCGCGGCGAGCACCGGATTTGACCGC 214732

Qy 867 GCCCTTCTGCTGCTCCAGGCTCTGCGGATCGCCTATGTGACAGCAAAAGGGGCTACCT 926
Db 214733 GCCGCTGTAGTGTGTCAGCGCACCGATGACCGGCTGATCCCATCGAGGGCAGCGGTG 214792

Qy 927 CTTATGAGGTAGCAAGAGCCAGGACAACTCTCAAGATTTATGAGTGTGCTACCA 986
Db 214793 CTTGTCGAATGTGTGGGATCGGCGGACGTGAGGATATCCCGGGCTGTACCA 214852

Qy 987 TGTCTCCACAGGAGC 1003
Db 214853 CGAGGTGTTCAACGAGC 214869

RESULT 5

US-09-060-756-652
Sequence 652, Application US/09060756
Patent No. 6183957
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060.756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 652
LENGTH: 402
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
NAME/KEY: unsure
LOCATION: (various positions within the sequence)
OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-652

Query Match 4.3%; Score 51.2; DB 3; Length 402;
Best Local Similarity 45.9%; Pred. No. 0.00014;
Matches 152; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 673 AAAGTGTCAACCTTGTGTCGCCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTC 732
Db 55 AAGCTTCTGGCGCTGCTGGTGGCCGCTCGCGTGCAGGAACCTGGATTTTACTGCCATC 114

Qy 733 TCTCGAATAAGACAGAGTTCGACATTTATACTCAGACCCCTGATCGCGGGCAGGG 792
Db 115 TCTCGACCTCGAGGTGGTCCAGGCTTACAACCCGACCCACTCGTGACACCGAGCG 174

Qy 793 CTGAAGTGTGCTTTCGGCATCCAACTGCTGAATCCGCTCTCACGGGTGGAGCGGCCCTC 852
Db 175 GTTCCGCGCGGATTTGCGCGGCTGCTGCANGTGGCGGAGACCATGCGCGGCGANCA 234

Qy 853 CCCAAGCTGATGTGCCCTTCTGCTGCTCCAGGGCTCTGCGGATCGCTATGTGACAGC 912
Db 235 CCGCATTTACCGCGCGCTGCTAGTGTGTCACGCGCACCGATGACCGGCTGATCCCCATC 294

Qy 913 AAAGGGCTTACCTGCTCATGGAGTTAGCCAAGAGCCAGGACAGACTCTCAAGATTTAT 972
Db 295 GAAGGAGCGCTCGCCTGGTCTGNAATGTTNGGATCNGCCGACGTCGACNTGAANGANTAT 354

Qy 973 GAAGGTGCTTACCATGTTCTCCCAAGGAGC 1003
Db 355 CCCCGCTGTNCCACNAGGTGTTCAACGAAC 385

RESULT 6
US-09-314-652
Sequence 652, Application US/09670314
Patent No. 6492506
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/670.314
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/060.756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 652
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-652

Query Match
Best Local Similarity 4.3%; Score 51.2; DB 4; Length 402;
Matches 152; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 673 AAAGTGCTCAACCTTGCTGCCAAACTGTGCTCCGGCCCATCGACTCCAGGCTGTC 732
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 733 TCTCGGAATAGACAGAGGTGACATTTATTAAGTCAAGACCCCTGATCTGCCGGGCGAGG 792
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 115 TCTCGGACCTTGAGGTGCTCCAGGCTTACAAACCGGACCCACTCGTGCACACGAGCG 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 793 CTGAAGGTGCTCTCGGCATCCAACTGCTGAATGCGGTCTCACGGTGGAGCGCCCTC 852
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 175 GTTCGGCCGGGATGTCGGCGGCTGCTGCANGTGGCGGAGACCATGCCCGGGGANCA 234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 853 CCCAAGTGACTGTGCCCTTCTCTGCTGCCAGGCTCTGCCGATCGCTATGTGACAGC 912
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 235 CCGGATTGACCGCGCGCTGCTAGTGTGCACGGCACCGGCTGATCCCCATC 294
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 913 AAAGGGCTACCTGCTCATGGAGTTAGCAAGACCGAGCAAGACTCTCAAGATTAT 972
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 295 GAAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 973 GAAGTGCTACCTGCTTCTCCAAAGGAGC 1003
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 355 CCCCGGCTGTCACNAGGTGTTCAACGAAC 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-540-1131
; Sequence 1131, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1131
; LENGTH: 15572
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-540-1131

Query Match
Best Local Similarity 4.1%; Score 48.4; DB 4; Length 15572;
Matches 162; Conservative 0; Mismatches 171; Indels 1; Gaps 1;

Qy 670 GCGAAAGTGCTCAACCTTGCTGCTCAAACTGTGCTCCGGGCCCATCGACTCCAGCGTG 729
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10115 GCGAAGATCTGCGGACGATTTCTCCCGGGTGTCCCGGCGAGGACTGGACGACGATG 10174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 730 CTCTCTCGGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGATCTGCCGGGCA 789
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10175 TTCCTGACGACGCGCGCGAGAGGAGCGGTTCCTCGGGATCCGCTCATCACCCACG-A 10233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 790 GGGCTGAAGTGTGCTTCCGGCATCCAACTGCTGAATGCGGTCTCACGGTGGAGCGGCC 849
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10234 GAGTGCCTCCGCGCTCCGCCAAGCGCTCATCCGCCCATCGAAGCGCTCGAGGGGAGG 10293
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 850 CTCCCAAGCTGACTGTGCCCTTCTCTGCTCCAGGGCTCTGCCGATCGCTATGTGAC 909
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10294 CTCAGGACCTTGAGACTCCCTCTGCTGCTGTCACGGGGCGGAGGAGCTCATCACCTCC 10353
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 910 AGCAAAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGACTCTCAAGATT 969
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10354 ATCGAAGCGAGCGCGCCCTGCTGGCGAGTCCACGATCGCGACAAGCGCTCATCATC 10413
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 970 TATGAAGTGTGCTACCATGTTCTCCACAAGAGC 1003
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10414 TACGAGGGCCAGCGCCACGATCTCGCGCACGAAC 10447
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-252-991A-5873/c
; Sequence 5873, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5873
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5873

Query Match
Best Local Similarity 3.6%; Score 43.4; DB 4; Length 534;
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 387 CTGCTGTGTTTCCGCCACGACATGTTGCCACGACAGAGCGAAGGGGAGAGATGTT 446
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 404 CTTCCAGCGCGTGTCCGCGGAGCAGCTCGGCTTTGCGCAGGGCGCGGAGAAACGAGT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 447 AGTGTCTGACTTCCACGTTTTTCGTACGGGATGTTTCAGCATGTGATTCATGCGAGAA 506
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 344 CGGCGCTGGCTCGACCTTCGCCAACGGCACCTGGTAGGTCTTGAACGACCCGTAGCGGA 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 507 AGACTACCTCGGGCTTCTGTTCTTCCTTC 535
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 284 AGCTTCTGCGGACATCATCCCTTCCTGC 256
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-252-991A-5829/c
; Sequence 5829, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 5829
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5829

Query Match 3.6%; Score 43.4; DB 4; Length 1968;
Best Local Similarity 55.7%; Pred. No. 0.055;
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 387 CTTGCTGGTTCGCCACGACCATGTTGGCCAGGACAGAGCGAAGGGGAGGATGGT 446
DB 1879 CTTCCAGCGCGTCCCGGAGCAGCTCGGCTTTCGCGAGGCGCGGAGAAACGCGAGT 1820
QY 447 AGTGTCTGACTTCCACGCTTTTGGTCAGGGATGTTGACGATGTCGATTCATGCAGAA 506
DB 1819 CGGCGTGGCTCGACCTTCGCCAACGCGACCTGGTAGGCTTGAACGCGACCGTAGCGGA 1760
QY 507 AGACTACCTGGGCTTCCTGTCTTCCTTC 535
DB 1759 AGCCTCGCTGGGCATCATCCTTCCTGC 1731

RESULT 10

US-09-252-991A-5779
; Sequence 5779, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5779
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5779

Query Match 3.6%; Score 43.4; DB 4; Length 2190;
Best Local Similarity 55.7%; Pred. No. 0.058;
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 387 CTTGCTGGTTCGCCACGACCATGTTGGCCAGGACAGAGCGAAGGGGAGGATGGT 446
DB 93 CTTCCAGCGCGTCCCGGAGCAGCTCGGCTTTCGCGAGGCGCGGAGAAACGCGAGT 152
QY 447 AGTGTCTGACTTCCACGCTTTTGGTCAGGGATGTTGACGATGTCGATTCATGCAGAA 506
DB 153 CGGCGTGGCTCGACCTTCGCCAACGCGACCTGGTAGGCTTGAACGCGACCGTAGCGGA 212
QY 507 AGACTACCTGGGCTTCCTGTCTTCCTTC 535
DB 213 AGCCTCGCTGGGCATCATCCTTCCTGC 241

RESULT 11

US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 3.3%; Score 39; DB 4; Length 832;
Best Local Similarity 8.9%; Pred. No. 0.65;
Matches 24; Conservative 135; Mismatches 110; Indels 0; Gaps 0;

QY 810 CATCCAACTCTCTCAATGCCGCTCTCACGGGTGGAGCGGCCTCCCCAAGCTGATGTGCC 869
DB 290 CMYRGRRCAWYTWARGMMSYAWGKWSMSMCTRMYYKGGSTYTWKCTCATWCYW 231
QY 870 CTTCTCTGCTCTCAGGGCTCTCCGATCGCTATGTGACGAGCAAAAGGGGCTACCTGCT 929
DB 230 YWYKWRMSKTCWSGSRGGYMTSYSTRSYMYWASWMTMCWWGRWHSYHYMWAGK 171
QY 930 CATGGAGTTAGCCAAGAGCCAGCAAGACTCTCAAGATTTATGAAGTGCCTTACCATGT 989
DB 170 KWRVATTWRRAMWMAWMTWMMWMAWCMSSRGAAMYRRTTMMWGYRYWKRKSYRR 111
QY 990 TCTCCAAAGGAGCTCTCGAAGTCACTCACTCGCTTCCATGAAATAAATGCTGGGT 1049
DB 110 TRCAWAYANKTKRSYTWCRWKRCMMMMMAVGYKTMWRACWKTRYRWMAWAMWR 51
QY 1050 CTCTCAAGAGCAGCCAGCGCAAGAACTG 1078
DB 50 MWWTMMMYTWYWRAMKRRWWRKWSWS 22

RESULT 12

US-09-280-116-63/c
; Sequence 63, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-63

Query Match 3.3%; Score 39; DB 3; Length 865;
Best Local Similarity 46.8%; Pred. No. 0.86;
Matches 123; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 310 CTCATCTTTTGTGTCCATGGAGCGGAGAGACAGATGGCGCGCTATGAAGAGCTGGCTCGG 369
DB 430 CTACTCTCAGTTTGGACTGAGCCAAGGAAAACAGTGGCGCGCACACCTTGCTTGGCGCAG 371
QY 370 ATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACAGCAATGTTGCCACGCGACAGC 429
DB 370 AACCTGGAGGCCCGCTGATGTCGTATCGAGAATGCCAAAAACAGAAACAGAAAAAGC 311
QY 430 GAAGGGGAGGAGTAGTGTCTGACTTCCAGTTCCTTCAGGGATGTTGTCAGCAT 489
DB 310 CACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTTCAGCCGAATTTTGGGAGGTG 251

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Job time : 254 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 03:13:18 ; Search time 791 Seconds
(without alignments)
9777.320 Million cell updates/sec

Title: U67963

Perfect score: 1192

Sequence: 1 CCAGCCCAAGGCGAGGTC.....CAAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 324468913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
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- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
- 22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1192	100.0	1192	9	US-09-880-107-3409
2	1192	100.0	1192	16	Sequence 3409, Ap
3	1192	100.0	1192	17	Sequence 7, Appli
4	1192	100.0	1192	17	Sequence 17, Appl
5	1192	100.0	1192	17	Sequence 17, Appl
6	1192	100.0	1192	19	US-10-647-426-15
7	1192	100.0	1192	19	US-10-775-169-231
					Sequence 231, App
					Sequence 673, App

8	1192	100.0	1582	21	US-10-956-157-1759	Sequence 1759, Ap
9	1162	97.5	4193	16	US-10-240-965-141	Sequence 141, App
10	1002	84.1	1309	21	US-10-498-788-49	Sequence 49, Appl
11	942	79.0	942	16	US-10-303-664A-8	Sequence 8, Appli
12	791.8	66.4	895	16	US-10-093-463-175	Sequence 175, App
13	749	62.8	861	17	US-10-093-463-177	Sequence 177, App
14	749	62.8	861	17	US-10-099-322-321	Sequence 321, App
15	667.2	56.0	912	21	US-10-764-420-209	Sequence 209, App
16	588	49.3	600	21	US-10-956-157-6994	Sequence 6994, Ap
17	519.8	43.6	556	10	US-09-918-995-29218	Sequence 29218, A
18	474.6	39.8	681	21	US-10-764-420-136	Sequence 136, App
19	417	35.0	452	10	US-09-918-995-32498	Sequence 32498, A
20	364.8	30.6	425	10	US-09-918-995-7833	Sequence 7833, Ap
21	306.4	25.7	463	10	US-09-918-995-23507	Sequence 23507, A
22	210.6	17.7	501	10	US-09-918-995-10625	Sequence 10625, A
23	204.2	17.1	376	9	US-09-728-445-419	Sequence 419, App
24	200	16.8	243	11	US-09-969-034-4029	Sequence 4029, Ap
25	198.4	16.6	506	9	US-09-917-800A-696	Sequence 696, App
26	116.2	9.7	837	17	US-10-282-122A-28443	Sequence 28443, A
27	116.2	9.7	972	17	US-10-282-122A-28166	Sequence 28166, A
28	113	9.5	831	17	US-10-282-122A-25663	Sequence 25663, A
29	94.4	7.9	644	13	US-10-027-632-114757	Sequence 114757,
30	94.4	7.9	644	17	US-10-027-632-114757	Sequence 114757,
31	84.8	7.1	825	17	US-10-369-493-28150	Sequence 28150, A
32	84.8	7.1	825	17	US-10-369-493-30910	Sequence 30910, A
33	84.8	7.1	903	17	US-10-282-122A-13068	Sequence 13068, A
34	80.8	6.8	1590	20	US-10-739-930-2161	Sequence 2161, Ap
35	75.8	6.4	928	20	US-10-425-115-74280	Sequence 74280, A
36	74.8	6.3	1665	18	US-10-425-115-14081	Sequence 14081, A
37	74.8	6.3	2637	20	US-10-425-115-101074	Sequence 101074,
38	71.4	6.0	840	17	US-10-282-122A-27862	Sequence 27862, A
39	70.8	5.9	946	19	US-10-437-963-97729	Sequence 97729, A
40	70.4	5.9	2619	20	US-10-357-930-23110	Sequence 23110, A
41	70.4	5.9	2619	20	US-10-357-930-28980	Sequence 28980, A
42	68.4	5.7	673	19	US-10-767-701-29426	Sequence 29426, A
43	66.2	5.6	909	17	US-10-282-122A-14592	Sequence 14592, A
44	65.6	5.5	927	17	US-10-369-493-24361	Sequence 24361, A
45	65	5.5	1476	20	US-10-425-115-128760	Sequence 128760,

ALIGNMENTS

RESULT 1
US-09-880-107-3409
; Sequence 3409, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3409
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U67963
US-09-880-107-3409

Query Match 100.0%; Score 1192; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCAGCCGAAAGGAGGGTCTGGGTGCGGGAAGAGGGCTCGAGCTGCTTCTCTGCTGCC 60
Qy 61 TTGGGGCGCCGATGAGGGAACAGCCGATTTGGCTGGTTCGTGATTTCTCCAGGCTGTC 120
Db 61 TTGGGGCGCCGATGAGGGAACAGCCGATTTGGCTGGTTCGTGATTTCTCCAGGCTGTC 120
Qy 121 GTGGTTGTGGAATCAAAAGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 121 GTGGTTGTGGAATCAAAAGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 180
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Db 241 CACCTGGTCAATGACAGCGACAGTACTCTTCTGCAAGTACTGGAACCCACAGGCACA 300
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCGGAGAGCACAGTGGCGGCTATGAAG 360
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Qy 421 GGACAGAGCGAAGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480
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Qy 781 TGCCGGGCGAGGGCTGAAGGTGCTTCGGCATCAACTGCTGATGCGCTCTCACGGGTG 840
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RESULT 2
US-10-303-664A-7
; Sequence 7, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; FILE REFERENCE: MPI2001-290P3R(M)
; CURRENT APPLICATION NUMBER: US/10/303,664A
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(1092)
US-10-303-664A-7
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Query Match 100.0%; Score 1192; DB 16; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 CACCTGGTCAATGACAGCGACAGTACTCTTCTGCAAGTACTGGAACCCACAGGCACA 300
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCGGAGAGCACAGTGGCGGCTATGAAG 360
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCGGAGAGCACAGTGGCGGCTATGAAG 360
Qy 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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Qy 421 GGACAGAGCGAAGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480
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Db	1141	AAGGCGAGATGGCTTCTCAGATATGGCTTGCAAAAAA	1192
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; Sequence 17, Application US/10044564			
; Publication No. US20040018196A1			
; GENERAL INFORMATION:			
; APPLICANT: Mezes et al.			
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same			
; FILE REFERENCE: 21402-240			
; CURRENT APPLICATION NUMBER: US/10/044,564			
; CURRENT FILING DATE: 2002-09-09			
; PRIOR APPLICATION NUMBER: 60/261,014			
; PRIOR FILING DATE: 2001-01-11			
; PRIOR APPLICATION NUMBER: 60/261,018			
; PRIOR FILING DATE: 2001-01-11			
; PRIOR APPLICATION NUMBER: 60/318,410			
; PRIOR FILING DATE: 2001-09-10			
; PRIOR APPLICATION NUMBER: 60/261,013			
; PRIOR FILING DATE: 2001-01-11			
; PRIOR APPLICATION NUMBER: 60/261,026			
; PRIOR FILING DATE: 2001-01-11			
; PRIOR APPLICATION NUMBER: 60/261,029			
; PRIOR FILING DATE: 2001-01-11			
; PRIOR APPLICATION NUMBER: 60/313,170			
; PRIOR FILING DATE: 2001-08-17			
; NUMBER OF SEQ ID NOS: 306			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 17			
; LENGTH: 1192			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-044-564-17			
Query Match 100.0%; Score 1192; DB 17; Length 1192;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCAGCCGAAAGGAGGCTTGGGTGCGGGAAGAGGCTCGGAGCTGCTTCTGCTGCC	60
Db	1	CCAGCCGAAAGGAGGCTTGGGTGCGGGAAGAGGCTCGGAGCTGCTTCTGCTGCC	60
Qy	61	TGGGGCGCCAGATGAGGAAACAGCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC	120
Db	61	TGGGGCGCCAGATGAGGAAACAGCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC	120
Qy	121	GTGGTTGGATGCARACGCGACACATATGGAACAGGACCTGAGACCTTCCAGC	180
Db	121	GTGGTTGGATGCARACGCGACACATATGGAACAGGACCTGAGACCTTCCAGC	180
Qy	181	ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACCGAGCTCCCT	240
Db	181	ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACCGAGCTCCCT	240

Qy	241	CACCTGCTCAATGACAGCAGACAGTACCTCTTCTGCAGGTACTTGGAAACCCACAGGCACA	300
Db	241	CACCTGCTCAATGACAGCAGACAGTACCTCTTCTGCAGGTACTTGGAAACCCACAGGCACA	300
Qy	301	CCCAAGGCCCTCATCTTTTGTGTCCTGAGAGCGGAGAGCAGTGGCCGCTATGAAGAG	360
Db	301	CCCAAGGCCCTCATCTTTTGTGTCCTGAGAGCGGAGAGCAGTGGCCGCTATGAAGAG	360
Qy	361	CTGGCTCGATGCTGATGCGGCTGGACCTGCTGGTGTTCGCCCAACCATGTTGGCCAC	420
Db	361	CTGGCTCGATGCTGATGCGGCTGGACCTGCTGGTGTTCGCCCAACCATGTTGGCCAC	420
Qy	421	GGACAGAGCAAGGGGAGAGATGCTGACTTCCACGTTTTCTGTCAGGATGTG	480
Db	421	GGACAGAGCAAGGGGAGAGATGCTGACTTCCACGTTTTCTGTCAGGATGTG	480
Qy	481	TTGCAGCATGTGGATTCATGCGCAAGAAAGACTACCTGGGCTTCTGCTTCTTCTGGGC	540
Db	481	TTGCAGCATGTGGATTCATGCGCAAGAAAGACTACCTGGGCTTCTGCTTCTTCTGGGC	540
Qy	541	CATCTCCATGGAGGCGCCATCGCCATCCTCAACGCGCAGAGAGGCGGGCCACTTCGCC	600
Db	541	CATCTCCATGGAGGCGCCATCGCCATCCTCAACGCGCAGAGAGGCGGGCCACTTCGCC	600
Qy	601	GGCATGCTACTCATTTGCGCTCTGGTTCTTCCCAATCCTGAATCTGCAACAACTTTCAAG	660
Db	601	GGCATGCTACTCATTTGCGCTCTGGTTCTTCCCAATCCTGAATCTGCAACAACTTTCAAG	660
Qy	661	GTCTCTGCTGCGAAAGTGCTCAACTTGTGCTGCGCAAACTTGTCCCTCGGGCCCATCGAC	720
Db	661	GTCTCTGCTGCGAAAGTGCTCAACTTGTGCTGCGCAAACTTGTCCCTCGGGCCCATCGAC	720
Qy	721	TCCAGCGTCTCTCTCGGAATAAGACAGAGGTGACATTTATACTCAGACCCCTGATC	780
Db	721	TCCAGCGTCTCTCTCGGAATAAGACAGAGGTGACATTTATACTCAGACCCCTGATC	780
Qy	781	TGCGGGGCGGCTGAGGTGCTTCCGCGATCCACTGCTGAATGCGCTCTCACGGGTG	840
Db	781	TGCGGGGCGGCTGAGGTGCTTCCGCGATCCACTGCTGAATGCGCTCTCACGGGTG	840
Qy	841	GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTCCAGGGCTCTGCGGATCGC	900
Db	841	GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTCCAGGGCTCTGCGGATCGC	900
Qy	901	CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGGTTAGCAAGAGCCAGGACAAGACT	960
Db	901	CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGGTTAGCAAGAGCCAGGACAAGACT	960
Qy	961	CTCAAGATTTATGAAGTGGCTTACCATGTTCTCCACAAAGGAGCTTCTGAGTCACCAAC	1020
Db	961	CTCAAGATTTATGAAGTGGCTTACCATGTTCTCCACAAAGGAGCTTCTGAGTCACCAAC	1020
Qy	1021	TCCGCTTTCCATGAATAAATGAGTGGGTCTCTCAAAAGGACAGCCACGGCAGGAACTGCG	1080
Db	1021	TCCGCTTTCCATGAATAAATGAGTGGGTCTCTCAAAAGGACAGCCACGGCAGGAACTGCG	1080
Qy	1081	TCCCAACCTTGAATGCAATGCGCGGTGCCGGCTCATGCTGCGGGGATGACGACGAGGG	1140
Db	1081	TCCCAACCTTGAATGCAATGCGCGGTGCCGGCTCATGCTGCGGGGATGACGACGAGGG	1140
Qy	1141	AAGGCGAGATGGCTTCTCAGATATGGCTTGCAAAAAA	1192
Db	1141	AAGGCGAGATGGCTTCTCAGATATGGCTTGCAAAAAA	1192
RESULT 5			
US-10-647-426-15			
; Sequence 15, Application US/10647426			
; Publication No. US20040110197A1			
; GENERAL INFORMATION:			
; APPLICANT: Skinner, Michael K.			
; APPLICANT: Patton, Jodi L.			

;; TITLE OF INVENTION: A METHOD OF DETERMINING TUMOR CHARACTERISTICS BY
;; TITLE OF INVENTION: DETERMINING ABNORMAL COPY NUMBER OR EXPRESSION LEVEL OF
;; TITLE OF INVENTION: LIPID-ASSOCIATED GENES
;; FILE REFERENCE: PATRICK EAGLEMAN: EMBOL-X 252/124
;; CURRENT APPLICATION NUMBER: US/10/647,426
;; CURRENT FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: US/09/676,052
;; PRIOR FILING DATE: 2000-09-28
;; NUMBER OF SEQ ID NOS: 95
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 15
;; LENGTH: 1192
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: gene
;; LOCATION: (1) .. (1192)
;; OTHER INFORMATION: The sequence of the cDNA coding for Human
;; OTHER INFORMATION: Lysophospholipase Homolog
US-10-647-426-15

Query Match 100.0%; Score 1192; DB 19; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGGGCTCGAGCTGCCTTCTCTGCTGCC 60
Db 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGGGCTCGAGCTGCCTTCTCTGCTGCC 60

Qy 61 TTGGGGCGGCCAGATGAGGAAACAGCCCGATTTGGCTTGTCTGATTTCTCAGGCTGTC 120
Db 61 TTGGGGCGGCCAGATGAGGAAACAGCCCGATTTGGCTTGTCTGATTTCTCAGGCTGTC 120

Qy 121 GTGGTGTGGAATGCAACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180
Db 121 GTGGTGTGGAATGCAACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240
Db 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240

Qy 241 CACTGTGTCATATGAGAGGAGCAGTACTCTTCTGAGGCTACTGGAACCCACAGGACCA 300
Db 241 CACTGTGTCATATGAGAGGAGCAGTACTCTTCTGAGGCTACTGGAACCCACAGGACCA 300

Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGAGCACAGTGCCTATGAAGAG 360
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGAGCACAGTGCCTATGAAGAG 360

Qy 361 CTGGCTCGGATGTGATGGGCTGGACCTGCTGTGTGTTGCGCCACGACCATGTTGGCCAC 420
Db 361 CTGGCTCGGATGTGATGGGCTGGACCTGCTGTGTGTTGCGCCACGACCATGTTGGCCAC 420

Qy 421 GGACAGAGCGAAGGGGAGAGATGGTATGTCTGACTTCCAGTTTTCGTGAGGATGTG 480
Db 421 GGACAGAGCGAAGGGGAGAGATGGTATGTCTGACTTCCAGTTTTCGTGAGGATGTG 480

Qy 481 TTGCAGCATGTGGATTCATGCAAGAAAGACTACCTGGGCTTCCTGCTTCTCTGGGC 540
Db 481 TTGCAGCATGTGGATTCATGCAAGAAAGACTACCTGGGCTTCCTGCTTCTCTGGGC 540

Qy 541 CACTTCCATGGAGGCGCATCGCCATCTCTACGCGCGCAGAGAGCGGGGCACTTCGCC 600
Db 541 CACTTCCATGGAGGCGCATCGCCATCTCTACGCGCGCAGAGAGCGGGGCACTTCGCC 600

Qy 601 GGCATGTACTCATTTCCGCTCTGGTCTTGGCCAACTCTGAATCTGCAACAACTTTCAAG 660
Db 601 GGCATGTACTCATTTCCGCTCTGGTCTTGGCCAACTCTGAATCTGCAACAACTTTCAAG 660

Qy 661 GTCCTTCTGCGAAAGTGTCTCAACTTGTGTCGCAAACTTGTCCCTCGGGCCCATCGAC 720
Db 661 GTCCTTCTGCGAAAGTGTCTCAACTTGTGTCGCAAACTTGTCCCTCGGGCCCATCGAC 720

Qy 721 TCAGCGGTGCTCTCTCGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGATC 780
Db 721 TCAGCGGTGCTCTCTCGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGATC 780

Qy 781 TGCGGGGCGAGGCTGAGGTGCTTTCGGCATCCACTGCTGAATGCCCTCTCAGGGTG 840
Db 781 TGCGGGGCGAGGCTGAGGTGCTTTCGGCATCCACTGCTGAATGCCCTCTCAGGGTG 840

Qy 841 GAGCGGCGCCCTCCCAAGCTGACTGTGCTCCCTTCTCTGCTGCTCCAGGGCTCTGCGGATCGC 900
Db 841 GAGCGGCGCCCTCCCAAGCTGACTGTGCTCCCTTCTCTGCTGCTCCAGGGCTCTGCGGATCGC 900

Qy 901 CTATGTGACAGCAAAAGGGCTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960
Db 901 CTATGTGACAGCAAAAGGGCTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960

Qy 961 CTCAAGNTTATGAAGTGCCTACCATGTTCTCCACAAGAGCTTCTGAGTCAACCAAC 1020
Db 961 CTCAAGNTTATGAAGTGCCTACCATGTTCTCCACAAGAGCTTCTGAGTCAACCAAC 1020

Qy 1021 TCCGCTTTCATGAAATAAATCATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080
Db 1021 TCCGCTTTCATGAAATAAATCATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080

Qy 1081 TCCCAACCTTGAATGCAATGCGCGGTGCCCGGTCTCATGGTCTGGGGGATGCGAGGAG 1140
Db 1081 TCCCAACCTTGAATGCAATGCGCGGTGCCCGGTCTCATGGTCTGGGGGATGCGAGGAG 1140

Qy 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGAAAAA 1192
Db 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGAAAAA 1192

RESULT 6
US-10-775-169-231
; Sequence 231, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-231

Query Match 100.0%; Score 1192; DB 19; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGGGCTCGAGCTGCCTTCTCTGCTGCC 60
Db 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGGGCTCGAGCTGCCTTCTCTGCTGCC 60

Qy 61 TTGGGGCGGCCAGATGAGGAAACAGCCCGATTTGGCTTGTCTGATTTCTCAGGCTGTC 120
Db 61 TTGGGGCGGCCAGATGAGGAAACAGCCCGATTTGGCTTGTCTGATTTCTCAGGCTGTC 120

Qy 121 GTGGTGTGGAATGCAACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180
Db 121 GTGGTGTGGAATGCAACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240
Db 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240

181 ATGCCAGAGGAAAGTTCCCCAGGCGGACCCCGCAGAGCAATTCCCTACCAGGACCTCCCT 240
241 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300
241 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300
301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360
301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360
361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACGACCAATGTTGGCCAC 420
361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACGACCAATGTTGGCCAC 420
421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTCCACGCTTTTCGTCAGGGATGTG 480
421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTCCACGCTTTTCGTCAGGGATGTG 480
481 TTGACAGATGTGGATTCCATGCAGAAAGACTPACCTGGGCTTCTGCTTCTCTTCTGGGC 540
481 TTGACAGATGTGGATTCCATGCAGAAAGACTPACCTGGGCTTCTGCTTCTCTTCTGGGC 540
541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCGCGGGCCACTTCGCC 600
541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCGCGGGCCACTTCGCC 600
601 GGCATGCTACTCATTTGGCCTCTGGTCTTGGCCAACTTGTCCCTCGGSCCCATCGAC 660
601 GGCATGCTACTCATTTGGCCTCTGGTCTTGGCCAACTTGTCCCTCGGSCCCATCGAC 660
661 GTCCTTGTGCGAAAGTGCTCAACCTTGTGCTGCGCAAACTTGTCCCTCGGSCCCATCGAC 720
661 GTCCTTGTGCGAAAGTGCTCAACCTTGTGCTGCGCAAACTTGTCCCTCGGSCCCATCGAC 720
721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATATACTCAGACCCCTGATC 780
721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATATACTCAGACCCCTGATC 780
781 TGCCGGCAGGGCTGAAGGTGCTTGGGCATCCAACTGCTGTAATGCGGTCTCAGGGTG 840
781 TGCCGGCAGGGCTGAAGGTGCTTGGGCATCCAACTGCTGTAATGCGGTCTCAGGGTG 840
841 GAGCGCGCTTCCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTTGGCCGATCGC 900
841 GAGCGCGCTTCCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTTGGCCGATCGC 900
901 CTATGTGACAGAAAGGGGCTACTGCTCATGAGTTAGCAAGACCCAGCAAGACT 960
901 CTATGTGACAGAAAGGGGCTACTGCTCATGAGTTAGCAAGACCCAGCAAGACT 960
961 CTCAGATTTATGAAGTGTCTACCATGTTCTCCACAGGAGCTTCTGAGTCAACCAAC 1020
961 CTCAGATTTATGAAGTGTCTACCATGTTCTCCACAGGAGCTTCTGAGTCAACCAAC 1020
1021 TCCGCTCTTCCATGAATAAATGAGGTCTCTCAAGAGCAGCCAGGAGGAAGTGGC 1080
1021 TCCGCTCTTCCATGAATAAATGAGGTCTCTCAAGAGCAGCCAGGAGGAAGTGGC 1080
1081 TCCCCACCTGAAATGCAATGGCCGGTCCCGGCTCATGTTGTTGGGGATGACAGCAGGG 1140
1081 TCCCCACCTGAAATGCAATGGCCGGTCCCGGCTCATGTTGTTGGGGATGACAGCAGGG 1140
1141 AAGGGCAGAGATGGCTTCTCAGATATGCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1192
1141 AAGGGCAGAGATGGCTTCTCAGATATGCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1192

RESULT 7
US-10-755-889-673
; Sequence 673 Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 673
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-673

Query Match 100.0%; Score 1192; DB 19; Length 1582;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCCGAAAGGCAGGCTTGGGTGCGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC 60
DB 379 CCAGCCGAAAGGCAGGCTTGGGTGCGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC 438
QY 61 TTGGGCGCGCCAGATGAGGGAACAGCCGATTTGCTGCTGCTTCTGATTTCTCCAGGCTGC 120
DB 439 TTGGGCGCGCCAGATGAGGGAACAGCCGATTTGCTGCTGCTTCTGATTTCTCCAGGCTGC 498
QY 121 GTGCTTGTGAATGCAAAACGCGACACATATGAAACAGGACCTGAAGACCTTCCAGC 180
DB 499 GTGCTTGTGAATGCAAAACGCGACACATATGAAACAGGACCTGAAGACCTTCCAGC 558
QY 181 ATGCCAGAGAAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACCAGGACTCCCT 240
DB 559 ATGCCAGAGAAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACCAGGACTCCCT 618
QY 241 CACTGTGCTCAATGACAGCGGACAGTACTCTTCTGCAAGTACTGGAACCCACAGGCACA 300
DB 619 CACTGTGCTCAATGACAGCGGACAGTACTCTTCTGCAAGTACTGGAACCCACAGGCACA 678
QY 301 CCCAAGGCCCTCATCTTTGTGTCCTATGAGCGGAGAGCAGTGGCGCGCTATGAAGAG 360
DB 679 CCCAAGGCCCTCATCTTTGTGTCCTATGAGCGGAGAGCAGTGGCGCGCTATGAAGAG 738
QY 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTTCCGCCACGACCATGTTGGCCAC 420
DB 739 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTTCCGCCACGACCATGTTGGCCAC 798
QY 421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTCCACGCTTTCGTCAGGGATGTG 480
DB 799 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTTCACGCTTTCGTCAGGGATGTG 858
QY 481 TTGACAGATGTGGATTCCATGCAGAAAGACTTACCTGGGCTTCTGCTTCTCTGCTGCCG 540
DB 859 TTGACAGATGTGGATTCCATGCAGAAAGACTTACCTGGGCTTCTGCTTCTCTGCTGCCG 918
QY 541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCGCGGGCCACTTCGCC 600
DB 919 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCGCGGGCCACTTCGCC 978
QY 601 GGATGCTACTCATTTTCGCTCTGGTTCCTGCAATCTGAACTGCAACAACTTTCAAG 660
DB 979 GGATGCTACTCATTTTCGCTCTGGTTCCTGCAATCTGAACTGCAACAACTTTCAAG 1038
QY 661 GTCTTGTCTCGAAAGTGTCAACCTTGTGCTGCCAACTTGTCTTCTCGGGCCCATCGAC 720
DB 1039 GTCTTGTCTCGAAAGTGTCAACCTTGTGCTGCCAACTTGTCTTCTCGGGCCCATCGAC 1098
QY 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATATACTCAGACCCCTGATC 780
DB 1099 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATATACTCAGACCCCTGATC 1158

APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL Program
SEQ ID NO 141
LENGTH: 4193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 216063.17
NAME/KEY: unsure
LOCATION: 1626-1649
OTHER INFORMATION: a, t, c, g, or other
US-10-240-965-141

Query Match 97.5%; Score 1162; DB 16; Length 4193;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1	CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCTCTGCTGCC	60
Db	452	CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCTCTGCTGCC	511
Qy	61	TTGGGGCGCCGACATGAGGGAACAGCCGATTTGCCCTGGTTCGTGATCTCCAGGCTGTC	120
Db	512	TTGGGGCGCCGACATGAGGGAACAGCCGATTTGCCCTGGTTCGTGATCTCCAGGCTGTC	571
Qy	121	GTGGTTGTGGAATGAAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC	180
Db	572	GTGGTTGTGGAATGAAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC	631
Qy	181	ATGCCAGAGAAAGTTCCCGAGGGGACCCCGAGAGCATTCCTTACCAGGACTCCCT	240
Db	632	ATGCCAGAGAAAGTTCCCGAGGGGACCCCGAGAGCATTCCTTACCAGGACTCCCT	691
Qy	241	CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACT-GGAAACCCACAGGCAC	299
Db	692	CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACTGGAAACCCACAGGCAC	751
Qy	300	ACCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA	359
Db	752	ACCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA	811
Qy	360	GCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTTCGCCACGACCATGTTGGCCA	419
Db	812	GCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTTCGCCACGACCATGTTGGCCA	871
Qy	420	CGGACAGACCAAGGGAGAGATGTTAGTCTGTGACTTCCACAGTTTTCGTCAGGGATGT	479
Db	872	CGGACAGACCAAGGGAGAGATGTTAGTCTGTGACTTCCACAGTTTTCGTCAGGGATGT	931
Qy	480	GTTGCAGCATGGATTCATGACAGAAAGACTACCTGGGCTTCTGTCTTCTTCTGGG	539
Db	932	GTTGCAGCATGGATTCATGACAGAAAGACTACCTGGGCTTCTGTCTTCTTCTGGG	991
Qy	540	CCACTCCATGGAGCGCCATCGGCATCTCAGCGCCGACAGAGGCGCGGCCACTTCGC	599
Db	992	CCACTCCATGGAGCGCCATCGGCATCTCAGCGCCGACAGAGGCGCGGCCACTTCGC	1051
Qy	600	CGGATGCTACTCATTTTCGCTCTGTTCTTGGCAATCCTCAATCTGCAACAACCTTTCAA	659
Db	1052	CGGATGCTACTCATTTTCGCTCTGTTCTTGGCAATCCTCAATCTGCAACAACCTTTCAA	1111
Qy	660	GGTCTTGTCTCGAAAGTGCTCAACCTTGTGCTGCGCAAACTTGCTCCCTCGGGCCCATCGA	719
Db	1112	GGTCTTGTCTCGAAAGTGCTCAACCTTGTGCTGCGCAAACTTGCTCCCTCGGGCCCATCGA	1171

Qy	720	CTCCAGCGTCTCTCTCGGAATAAGACAGAGTTCGACATTTATTAACCTCAGACCCCTGAT	779
Db	1172	CTCCAGCGTCTCTCTCGGAATAAGACAGAGTTCGACATTTATTAACCTCAGACCCCTGAT	1231
Qy	780	CTGCCGGGCGAGGGCTGAAAGTGTGCTTCCGATCCAACTGCTGAATGCCGCTCTCACGGGT	839
Db	1232	CTGCCGGGCGAGGGCTGAAAGTGTGCTTCCGATCCAACTGCTGAATGCCGCTCTCACGGGT	1291
Qy	840	GGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTCTCTGCTCCAGGGCTTTCGCCGATCG	899
Db	1292	GGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTCTCTGCTCCAGGGCTTTCGCCGATCG	1351
Qy	900	CCTATGTGACAGCAAGGGGCTTACCTGCTCATGGAGTTAGCCCAAGAGCCAGGACAGAC	959
Db	1352	CCTATGTGACAGCAAGGGGCTTACCTGCTCATGGAGTTAGCCCAAGAGCCAGGACAGAC	1411
Qy	960	TCTCAAGATTTATGAAGTGTCTTACCATGTTCTCCAAAGAGGCTTCTTGAAGTCACCAA	1019
Db	1412	TCTCAAGATTTATGAAGTGTCTTACCATGTTCTCCAAAGAGGCTTCTTGAAGTCACCAA	1471
Qy	1020	CTCCGCTTCTCCATGAAATAAACATGTGGGTCTCTCAAAGACACGCCACGGCAGAACTGC	1079
Db	1472	CTCCGCTTCTCCATGAAATAAACATGTGGGTCTCTCAAAGACACGCCACGGCAGAACTGC	1531
Qy	1080	GTCCCCACCTCTGAATGCAATTTGGCCGGTCCCGGCTCATGGTCTGGGGGATGCAGGCAGG	1139
Db	1532	GTCCCCACCTCTGAATGCAATTTGGCCGGTCCCGGCTCATGGTCTGGGGGATGCAGGCAGG	1591
Qy	1140	GAAGGGCAGAGATGGCTTCTCAGATATGGCTTGC	1173
Db	1592	GAAGGGCAGAGATGGCTTCTCAGATATGGCTTGC	1625

RESULT 10
US-10-498-788-49
; Sequence 49, Application US/10498788
; Publication No. US20050118594A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Narinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Lee, Ernestine A.
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Khare, Reena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Erika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April J. A.
; APPLICANT: Jin, Pei
; APPLICANT: Swarnakar, Anita
; APPLICANT: Li, Joana X.
; APPLICANT: Marquis, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; APPLICANT: Elliott, Vicki S.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1312 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/343,558
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/351,107

;; PRIOR FILING DATE: 2002-01-22
;; NUMBER OF SEQ ID NOS: 84
;; SOFTWARE: PERL Program
;; SEQ ID NO 49
;; LENGTH: 1309
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc feature
;; OTHER INFORMATION: incyte ID No: 7505864CB1
US-10-498-788-49

Query Match 84.1%; Score 1002; DB 21; Length 1309;
Best Local Similarity 92.4%; Pred. No. 2.1e-305;
Matches 1102; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

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Qy 1 CCAGCCGAAAGGAGGCTCTGGGTGGGGAAGAGGCTCGAGCTCGCTTCCTGCTGCC 60
Db 206 CCAGCCGAAAGGAGGCTCTGGGTGGGGAAGAGGCTCGAGCTCGCTTCCTGCTGCC 265
Qy 61 TTGGGGCCGCCAGATGAGGGAACAGCCGATTTGCTGGTTCTGATTCTCCAGGCTGTC 120
Db 266 TTGGGGCCGCCAGATGAGGGAACAGCCGATTTGCTGGTTCTGATTCTCCAGGCTGTC 325
Qy 121 GTGGTTGTGGAATCAAAACGACGACATATGGAACAGAGACCTTGAGACCTTCCAGC 180
Db 326 GTGGTTGTGGAATCAAAACGACGACATATGGAACAGAGCTTGAGACCTTCCAGC 385
Qy 181 ATGCAGAGGAAAGTTCCCGAGGGGACCCCGAGAGCATTCCTTACAGGACCTCCCT 240
Db 386 ATGCAGAGGAAAGTTCCCGAGGGGACCCCGAGAGCATTCCTTACAGGACCTCCCT 445
Qy 241 CACCTGTCTAATGAGAGGACGACTCTCTCTGCAAGTACTGGAACCCACAGGCACA 300
Db 446 CACCTGTCTAATGAGAGGACGACTCTCTCTGCAAGTACTGGAACCCACAGGCACA 505
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGGACAGCAGTGGCGCTATGAAG 360
Db 506 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGGACAGCAGTGGCGCTATGAAG 565
Qy 361 CTGCTCTGATGATGGGGCTGACCTGTGTGTGTGGCCACAGCATTGTTGGCCAC 420
Db 566 CTGCTCTGATGATGGGGCTGACCTGTGTGTGTGGCCACAGCATTGTTGGCCAC 625
Qy 421 GGACAGAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTCAGGAGTGT 480
Db 626 GGACAGAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTCAGGAGTGT 685
Qy 481 TTGAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCTTCTGGC 540
Db 686 TTGAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCTTCTGGC 745
Qy 541 CACTCCATGGAGGCGGCATCGCCATCTCAACGCGCGAGAGAGCGCGGCGCACTTGGC 600
Db 746 CACTCCATGGAGGCGGCATCGCCATCTCAACGCGCGAGAGAGCGCGGCGCACTTGGC 805
Qy 601 GGCATGTACTCATTTGCTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 806 GGCATGTACTCATTTGCTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
Qy 661 GTCCTTGTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTGCTCGGCGCCATCGAC 720
Db 864 ----- 863
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATTAATCTAGACCCCTGATC 780
Db 864 -----AGTTCGACATTTATTAATCTAGACCCCTGATC 895
Qy 781 TGCCGGGAGGCGCTGAAGGTGTCTTGGGCATCCAACTGCTGAATGCCGCTCTCAGGGTG 840
Db 896 TGCCGGGAGGCGCTGAAGGTGTCTTGGGCATCCAACTGCTGAATGCCGCTCTCAGGGTG 955
Qy 841 GAGGGCGCCCTCCCAAGCTGACTGTGCTGCTTCTGCTGCTCCAGGGCTCTGCGGATCGC 900
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Db 956 GAGCGGCGCTCCCAAGCTGACTGTGCCCTTCTGCTGCCAGGCTCTGCCGATCGC 1015
Qy 901 CTATGTGACAGCAAAAGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGACT 960
Db 1016 CTATGTGACAGCAAAAGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGACT 1075
Qy 961 CTCAGAATTTATGAAGGTGCTTACCATGTTCTCCCAAGAGGCTTCTGAAGTCAACCAAC 1020
Db 1076 CTCAGAATTTATGAAGGTGCTTACCATGTTCTCCCAAGAGGCTTCTGAAGTCAACCAAC 1135
Qy 1021 TCCGCTTTCATGAATAAATGAGTGGGTCTCTCAAGAGGACAGCCAGGAGGACTGCG 1080
Db 1136 TCCGCTTTCATGAATAAATGAGTGGGTCTCTCAAGAGGACAGCCAGGAGGACTGCG 1195
Qy 1081 TCCCCACCTCTGAATGCAATGCGCGGTCCCGGCTCATGGTCTGGGGGATGCAGGCAGGG 1140
Db 1196 TCCCCACCTCTGAATGCAATGCGCGGTCCCGGCTCATGGTCTGGGGGATGCAGGCAGGG 1255
Qy 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAGGAGGAGGAGGAGG 1192
Db 1256 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAGGAGGAGGAGGAGG 1307
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RESULT 11

US-10-303-664A-8
; Sequence 8, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Teal, Fong-Ying
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; FILE REFERENCE: MPI2001-290P3R(M)
; CURRENT APPLICATION NUMBER: US/10/303,664A
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-664A-8

Query Match 79.0%; Score 942; DB 16; Length 942;
Best Local Similarity 100.0%; Pred. No. 1.7e-286;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 151 ATGAAACAGAGACCTGAAGACCTTCCAGATGTCAGAGGAAAGTTCCTCCAGCGGACC 210
Db 1 ATGAAACAGAGACCTGAAGACCTTCCAGATGTCAGAGGAAAGTTCCTCCAGCGGACC 60
Qy 211 CCGCAGAGCATTCCTTACCAGGACCTCCCTCACCTGTCATGTCAGAGGACAGTACCTC 270
Db 61 CCGCAGAGCATTCCTTACCAGGACCTCCCTCACCTGTCATGTCAGAGGACAGTACCTC 120
Qy 271 TTCTGCAAGTACTGGAACCCACAGGCACACCCAGGCCCTCATCTTTGTGTCATCGA 330
Db 121 TTCTGCAAGTACTGGAACCCACAGGCACACCCAGGCCCTCATCTTTGTGTCATCGA 180
Qy 331 GCCGAGAGACAGTGGCGGCTATGAAGAGCTGCTGGATGCTGATGGGCTGACCTG 390
Db 181 GCCGAGAGACAGTGGCGGCTATGAAGAGCTGCTGGATGCTGATGGGCTGACCTG 240
Qy 391 CTGCTGTTGCGCCACAGCACCATTGTTGGCCAGCAGAGGAGGAGGAGGATGTTAGTG 450
Db 241 CTGCTGTTGCGCCACAGCACCATTGTTGGCCAGCAGAGGAGGAGGAGGATGTTAGTG 300
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QY 451 TCTGACTTCCACGTTTTCGTTCAGGGATGTGTCAGCATGTGGATTCCATCAGAAAGAC 510
Db 301 TCTGACTTCCACGTTTTCGTTCAGGGATGTGTCAGCATGTGGATTCCATCAGAAAGAC 360
QY 511 TACCTCGGCTTCCTGTCTCTCTTCGGGCCACTCCATGGGAGGCGCCATCGCCATCCTC 570
Db 361 TACCTCGGCTTCCTGTCTCTCTTCGGGCCACTCCATGGGAGGCGCCATCGCCATCCTC 420
QY 571 ACGGCGCAGAGAGCCGGGCACTTCGCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 630
Db 421 ACGGCGCAGAGAGCCGGGCACTTCGCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 631 GCCAATCTGATCTGCAACAACCTTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 690
Db 481 GCCAATCTGATCTGCAACAACCTTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 691 CTGCCAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 750
Db 541 CTGCCAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 600
QY 751 GTCGACATTTAATCTAGACCCCTGATCTGCGGGCAGGGCTGAAGGTGTCTTCGGC 810
Db 601 GTCGACATTTAATCTAGACCCCTGATCTGCGGGCAGGGCTGAAGGTGTCTTCGGC 660
QY 811 ATCAACTGCTGAATGCGTCTCACGGTGGAGCGGCCCTCCCAAGCTGACTGTGCC 870
Db 661 ATCAACTGCTGAATGCGTCTCACGGTGGAGCGGCCCTCCCAAGCTGACTGTGCC 720
QY 871 TTCCTGCTCTCCAGGCTCTGCGCATCGCTATGTGACCAAAAGGGGCTACTGTCTC 930
Db 721 TTCCTGCTCTCCAGGCTCTGCGCATCGCTATGTGACCAAAAGGGGCTACTGTCTC 780
QY 931 ATGAGTTAGCCAGAGCCAGCAAGACTCTCAAGATTTATGAAGTGCTTACCATGTT 990
Db 781 ATGAGTTAGCCAGAGCCAGCAAGACTCTCAAGATTTATGAAGTGCTTACCATGTT 840
QY 991 CTCACAGGAGCTCTCTGAAGTCACCAACTCCGCTCTCCATGAATAAATATGCGGTC 1050
Db 841 CTCACAGGAGCTCTCTGAAGTCACCAACTCCGCTCTCCATGAATAAATATGCGGTC 900
QY 1051 TCTCAAAGGACAGCCAGGCAAGCTGCGTCCCAAGCCCTGA 1092
Db 901 TCTCAAAGGACAGCCAGGCAAGCTGCGTCCCAAGCCCTGA 942

RESULT 12
US-10-093-463-175
; Sequence 175, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
```

```
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypeptic
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 175
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(885)
US-10-093-463-175

Query Match 66.4%; Score 791.8; DB 17; Length 895;
Best Local Similarity 90.7%; Pred. No. 4.5e-239;
Matches 893; Conservative 0; Mismatches 2; Indels 90; Gaps 1;

QY 116 CTGTGCTGGTGTGGAAATGCAAAACGCCAGCACATAATGGAACACAGGACCTGAAGACCCCTT 175
Db 1 CTGTGCTGGTGTGGAAATGCAAAACGCCAGCACATAATGGAACACAGGACCTGAAGACCCCTT 60
QY 176 CCAGCATGCCAGAGAAAGTTCCCCAGGCGGACCCCGCAGAGCATTCCTTACCAGGACC 235
Db 61 CCAGCATGCCAGAGAAAGTTCCCCAGGCGGACCCCGCAGAGCATTCCTTACCAGGACC 120
QY 236 TCCTTCACCTGGTCAATGTCAGAGCGGACGAGTACCTCTTCTGCAGGTACTGGAAACCCACAG 295
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Query Match      62.8%; Score 749; DB 17; Length 861;
Best Local Similarity 90.4%; Pred. No. 1.5e-225;
Matches 849; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 151 ATGGAACAGGACCTGAAAGACCTTCCAGATGCGAGAGAAAGTTCCCCAGCGGACC 210
Db 7 ATGGAACAGGACCTGAAAGACCTTCCAGATGCGAGAGAAAGTTCCCCAGCGGACC 66

Qy 211 CCGCAGAGCATTCCTACCGAGCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 270
Db 67 CCGCAGAGCATTCCTACCGAGCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 126

Qy 271 TTCTGCAGTACTGGAACCCACAGGACACCAAGGCCCTCATCTTTGTCTCCATGGA 330
Db 127 TTCTGCAGTACTGGAACCCACAGGACACCAAGGCCCTCATCTTTGTCTCCATGGA 186

Qy 331 GCCGAGAGCAGTGGCCGCTATGAAGAGTGGCTCGATGCTGATGGGCTGAGACCTG 390
Db 187 GCCGAGAGCAGTGGCCGCTATGAAGAGTGGCTCGATGCTGATGGGCTGAGACCTG 246

Qy 391 CTGGTGTCCGCCAGCAGCATTTGGGCCACGACAGAGCGGAAGGAGAGGATGGTAGT 450
Db 247 CTGGTGTCCGCCAGCAGCATTTGGGCCACGACAGAGCGGAAGGAGAGGATGGTAGT 306

Qy 451 TCTGACTTCCACGTTTTCGTGAGGATGTTGCGAGCATGTGGATTCATGTCAGAAAGAC 510
Db 307 TCTGACTTCCACGTTTTCGTGAGGATGTTGCGAGCATGTGGATTCATGTCAGAAAGAC 366

Qy 511 TACCTGGGCTTCCCTGCTTTCTTTCTGGGCCACTTCCATGGGAGCGGCATCGCCATCCTC 570
Db 367 TACCTGGGCTTCCCTGCTTTCTTTCTGGGCCACTTCCATGGGAGCGGCATCGCCATCCTC 426

Qy 571 ACGCCCGCAGAGGCGCGGCCACTTCCCGGCATGCTACTCATTTGCGCTCTGGTCTT 630
Db 427 ACGCCCGCAGAGGCGCGGCCACTTCCCGGCATGCTACTCATTTGCGCTCTGGTCTT 486

Qy 631 GCCAATCTGAATCTGCAACAACTTTCAAGGTCCTTGCTGCGAAAGTGCTCAACCTTTGTG 690
Db 487 GCCAATCTGAATCTGCAACAACTTTCAAGGTCCTTGCTGCGAAAGTGCTCAACCTTTGTG 514

Qy 691 CTGCCAAACTTGTCCCTCGGSCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 750
Db 515 -----AG 516

Qy 751 GTCCACATTTATACTCAGACCCCTGATCTGCGGGCAGGGCTGAAGTGTGCTTCGGC 810
Db 517 GTCCACATTTATACTCAGACCCCTGATCTGCGGGCAGGGCTGAAGTGTGCTTCGGC 576

Qy 811 ATCCAACTGCTGAATGCGCTCTCACGGGTGGAGCGCGCCCTCCCAAGCTGACTGTGCC 870
Db 577 ATCCAACTGCTGAATGCGCTCTCACGGGTGGAGCGCGCCCTCCCAAGCTGACTGTGCC 636

Qy 871 TTCCTGTCTCCAGGGCTTCCCGATGCGCTATGTGACAGCAAGGGGCTTACCTGCTC 930
Db 637 TTCCTGTCTCCAGGGCTTCCCGATGCGCTATGTGACAGCAAGGGGCTTACCTGCTC 696

Qy 931 ATGGAGTTAGCAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGGCTTACCATGTT 990
Db 697 ATGGAGTTAGCAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGGCTTACCATGTT 756

Qy 991 CTCACAAAGAGACTTCTGGAAGTCAACAACTCCGCTTCCATGAAATAAATATGTTGGTGC 1050
Db 757 CTCACAAAGAGACTTCTGGAAGTCAACAACTCCGCTTCCATGAAATAAATATGTTGGTGC 816

Qy 1051 TCTCAAAGGACAGCCACGGCAGGAACCTGCGTCCCAACC 1089
Db 817 TCTCAAAGGACAGCCACGGCAGGAACCTGCGTCCCAACC 855
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RESULT 14

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US-10-099-322-321
; Sequence 321, Application US/10099322
; Publication No. US20030215449A1
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; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/10/099,322
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 321
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-099-322-321

Query Match      62.8%; Score 749; DB 17; Length 861;
Best Local Similarity 90.4%; Pred. No. 1.5e-225;
Matches 849; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 151 ATGGAACAGGACCTGAAAGACCTTCCAGATGCGAGAGAAAGTTCCCCAGCGGACC 210
Db 7 ATGGAACAGGACCTGAAAGACCTTCCAGATGCGAGAGAAAGTTCCCCAGCGGACC 66

Qy 211 CCGCAGAGCATTCCTACCGAGCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 270
Db 67 CCGCAGAGCATTCCTACCGAGCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 126

Qy 271 TTCTGCAGTACTGGAACCCACAGGACACCAAGGCCCTCATCTTTGTCTCCATGGA 330
Db 127 TTCTGCAGTACTGGAACCCACAGGACACCAAGGCCCTCATCTTTGTCTCCATGGA 186

Qy 331 GCCGAGAGCAGTGGCCGCTATGAAGAGTGGCTCGATGCTGATGGGCTGAGACCTG 390
Db 187 GCCGAGAGCAGTGGCCGCTATGAAGAGTGGCTCGATGCTGATGGGCTGAGACCTG 246

Qy 391 CTGGTGTCCGCCAGCAGCATTTGGGCCACGACAGAGCGGAAGGAGAGGATGGTAGT 450
Db 247 CTGGTGTCCGCCAGCAGCATTTGGGCCACGACAGAGCGGAAGGAGAGGATGGTAGT 306

Qy 451 TCTGACTTCCACGTTTTCGTGAGGATGTTGCGAGCATGTGGATTCATGTCAGAAAGAC 510
Db 307 TCTGACTTCCACGTTTTCGTGAGGATGTTGCGAGCATGTGGATTCATGTCAGAAAGAC 366

Qy 511 TACCTGGGCTTCCCTGCTTTCTTTCTGGGCCACTTCCATGGGAGCGGCATCGCCATCCTC 570
Db 367 TACCTGGGCTTCCCTGCTTTCTTTCTGGGCCACTTCCATGGGAGCGGCATCGCCATCCTC 426

Qy 571 ACGCCCGCAGAGGCGCGGCCACTTCCCGGCATGCTACTCATTTGCGCTCTGGTCTT 630
Db 427 ACGCCCGCAGAGGCGCGGCCACTTCCCGGCATGCTACTCATTTGCGCTCTGGTCTT 486

Qy 631 GCCAATCTGAATCTGCAACAACTTTCAAGGTCCTTGCTGCGAAAGTGCTCAACCTTTGTG 690
Db 487 GCCAATCTGAATCTGCAACAACTTTCAAGGTCCTTGCTGCGAAAGTGCTCAACCTTTGTG 514

Qy 691 CTGCCAAACTTGTCCCTCGGSCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 750
Db 515 -----AG 516
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QY 751 GTCGACATTTATACTCAGACCCCTGATCTCCCGGGCAGGGCTGAAGGTGTGCTTCGGC 810
Db 517 GTCGACATTTATACTCAGACCCCTGATCTCCCGGGCAGGGCTGAAGGTGTGCTTCGGC 576
QY 811 ATCCAACTGCTCAATGCGGTCTCAGGGGTGGAGCGCGCTCCCAAGTGAAGTGTGCCC 870
Db 577 ATCCAACTGCTCAATGCGGTCTCAGGGGTGGAGCGCGCTCCCAAGTGAAGTGTGCCC 636
QY 871 TTCCTGCTGCTCCAGGGTCTCCGATCGCCTATGTGACAGCAAAAGGGGCTTACCTGCTC 930
Db 637 TTCCTGCTGCTCCAGGGTCTCCGATCGCCTATGTGACAGCAAAAGGGGCTTACCTGCTC 696
QY 931 ATGGAGTTAGCCAAAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTTACCATGTT 990
Db 697 ATGGAGTTAGCCAAAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTTACCATGTT 756
QY 991 CTCACAGAGGAGCTCTTGAAGTCAACCACTCCGCTTCCATGAATAAATGAATGGGTC 1050
Db 757 CTCACAGAGGAGCTCTTGAAGTCAACCACTCCGCTTCCATGAATAAATGAATGGGTC 816
QY 1051 TCTCAAGGACAGCCAGCGCAAGAACTGCTGCCCCACCC 1089
Db 817 TCTCAAGGACAGCCAGCGCAAGAACTGCTGCCCCACCC 855

RESULT 15
US-10-764-420-209
; Sequence 209, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; FILE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-209

Query Match 56.0%; Score 667.2; DB 21; Length 912;
Best Local Similarity 83.2%; Pred. No. 1e-199;
Matches 759; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 181 ATGCCAGAGGAAGTTCCCGAGGGGACCCCGAGAGCAATTCCTACAGGACCTCCCT 240
Db 1 ATGCTGAGGCAAGTTACCCAGGGAAGTCCAGAGATGTTCCCTACAGGACCTGCT 60
QY 241 CACCTGGTCAATGACAGCGGACAGTACTTCTTGTGAGGTACTGGAACCCACAGGCACA 300
Db 61 CACCTGGTCAATGACAGCGGACAGTACTTCTTGTGAGGTACTGGAAGCCAGTGGCACA 120
QY 301 CCCAAGGCCCTCATCTTTGTCTCCATGAGCGGAGAGCAGTGGCGCTATGAAGAG 360
Db 121 CCCAAGGCCCTCATCTTTGTCTCCATGAGCTGGGAACACTGTGGCGGTTATGATGAG 180
QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGTGTCGCCACAGCACCATGTTGGCCAC 420
Db 181 CTGGCTCATATGTTGAAGGGGCTGGACATGCTGGTATTTGCCCATGACCATGTTGGCCAT 240
QY 421 GGACAGAGCGAAGGGGAGAGGATGATGTCTGACTTCCAGTTCCTGTCAGGGATGTG 480
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Db 241 GGGCAGAGTGAGGGAGAGAGGATGGTGGTGTGCGACTTCCAAGTTTTTGTGTCAGAGATGTG 300
QY 481 TTGCAGCATGTGGATTCCATGCGAGAAAGACTTACCCTGGGTTCCTGCTTCTTCTTCTGGGC 540
Db 301 CTGCAACAGGTGGACACATCCAGAGAGACTACCCCGACGTCCCCATCTTCTCTCTGGGC 360
QY 541 CACTTCCATGGAGGGCGCCATCGCCATCCTCACGGCCGACAGAGGGCGGGCCACTTCCGC 600
Db 361 CACTTCCATGGCGGTGCGCATCTCCATCTAGTGGCTGACAGAGAGGCCCAACCTACTTTTCT 420
QY 601 GGCATGCTACTCATTTTCGCTCTGGTCTTTCGCCAATCTGAACTGCAACAACTTTCAAG 660
Db 421 GGCATGCTCTGATTTTCACTCTGGTCTTTCGCCAATCCGGAATCTGCACTGCACTTTGAAG 480
QY 661 GTCCTTCTGCGAAAGTGTCTCAACCTTGTGCTGCCAAACTTGTCCCTCGGGCCCATCGAC 720
Db 481 GTCCTTCTGCGAAACTGCTCAATTTTGTCTGCCAATATGACCTTGGGGCGCATTTGAC 540
QY 721 TCCAGCGTGTCTCTTCGGAATAAGACAGAGGTGACATTTTAACTCAGACCCCTCGATC 780
Db 541 TCCAGCGTGTCTCTCGGAACAAGTGGAGGTTGACCTGTACAACTCTGACCCCACTCGTC 600
QY 781 TGCGGGCAGGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCCGTCTCAGGGTG 840
Db 601 TGCGGAGCAGGGCTGAAGGTGTGCTTTGGCATACAGCTGCTGAATGCCGTGCAAGAGTG 660
QY 841 GAGCGGCCCTCCCAAGCTGACTGTGSCCTTCTGCTGCTCCAGGGCTCTGCCGATCGC 900
Db 661 GAGCGAGCAATGCCAGGCTGACACTGCCATTTCTGCTGTCAGAGGTTCTGCTGACCGG 720
QY 901 CTATGTGACAGCAAAAGGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGACT 960
Db 721 CTTTGGCAGACAAAGGTGCTTACCTGCTCATGGAATCATCCCGAGTCAAGACAAAACA 780
QY 961 CTCAGATTTTATGAAGTGTGCTTACCATGTTCTCCAAAGAGGCTTCTGAAGTCAACCAAC 1020
Db 781 CTCAGATGTATGAAGTGTGCTTACCTGCTCCACAGGGAGCTTCCGGAAGTGAACCAAC 840
QY 1021 TCCGCTCTTCCATGAATAAATGAGTGGTCTCTCAAGGAGACAGCCAGCGAGGAACCTGCG 1080
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QY 1081 TCCCCACCCCTGA 1092
Db 901 TGTCCACCCCTGA 912
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